

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:35:58 ; Search time 1452.17 Seconds
(without alignments)
8655.682 Million cell updates/sec

Title: US-09-079-874-1

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Scoring table: IDENTITY NUC

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	257.8	88.9	373	6	BD024357	BD024357 Sequence
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4	236	81.4	946	9	HSA297436	AJ297436 Homo sapi
5	232.4	80.1	979	6	BD076397	BD076397 Human pro
6	227	78.3	990	6	AX014204	AX014204 Sequence
7	227	78.3	990	6	BD205072	BD205072 Human nuc
8	227	78.3	990	9	AF043498	AF043498 Homo sapi
9	227	78.3	998	6	AR162849	AR162849 Sequence
10	227	78.3	998	6	AR302232	AR302232 Sequence
11	227	78.3	998	6	AX080304	AX080304 Sequence
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34	112.4	38.8	2532	9	AK092432	AK092432 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 610 from Patent EP1033401.
ACCESSION AX884747
VERSION AX884747.1 GI:40040217
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 610 06-SEP-2000;

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ACCESSION        BD024357
VERSION          BD024357.1 GI:22565580
KEYWORDS         JP 2001269182-A/603.
SOURCE           Homo sapiens (human)
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Edwards,J.B.D.M., Duclait,E. and Jordan,J.Y.
TITLE            Sequence tag and encoded human protein
JOURNAL          Patent: JP 2001269182-A 603 02-OCT-2001;
COMMENT
CS Homo sapiens (human)
PN JP 2001269182-A/603
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
C12N5/10,
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PH Key Location/Qualifiers
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QY 61 AAGCGTGTCTGCTTGCCTTGTGATGCGAGCTTGGCCCTGCGAGCGAGCACTGCCCTG 120
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LOCUS             BD076969
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ACCESSION        BD076969
VERSION          BD076969.1 GI:22622572
KEYWORDS         JP 2001512013-A/216.
SOURCE           Homo sapiens (human)
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE            5' EST of secretory protein expressed in prostate
JOURNAL          Patent: JP 2001512013-A 216 21-AUG-2001;
COMMENT
CS Homo sapiens (human)
PN JP 2001512013-A/216
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C07K14/47,C12P21/02,C12Q1/02,C12Q1/68,C12N15/00,CC
blastn
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CC region 404..466
CC id AA158879
CC est
CC Von Heijne matrix
CC score 7.5
CC seq AVLLALLMAGLAL/QP
CC n-a, S, C or t
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FT misc feature 72..73.
FT Location/Qualifiers
FT 1..373
FT /organism="Homo sapiens"

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ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 990)
AUTHORS Reiter,R.E., Gu,Z., Watabe,T., Thomas,G., Kinga,S., Davis,E.,
Wahl,M., Nisitani,S., Yamashiro,J., Le Beau,M.M., Lossa,M. and
Witte,O.N.
TITLE Prostate stem cell antigen: a cell surface marker overexpressed in
prostate cancer
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (4), 1735-1740 (1998)
MEDLINE 98132661
PUBMED 9465086
REFERENCE 2 (bases 1 to 990)
AUTHORS Reiter,R.E.
DIRECT SUBMISSION
TITLE Submitted (19-JAN-1998) Urology, UCLA, 66-134 CHS 10833 Le Conte
JOURNAL Ave., Los Angeles, CA 90095, USA
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DB 190 TCCTGACCGTCATCAGCAAAAGGCTGCAGTTGAATCGCTGGATGANTCAGAGGANTACT 249

QY 289 AC 290
DB 250 AC 251

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AR302232
LOCUS AR302232 998 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6541212.
ACCESSION AR302232
VERSION AR302232.1 GI:31690451
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 998)
AUTHORS Reiter,R.E. and Witte,O.N.
TITLE Methods for detecting prostate stem cell antigen protein
JOURNAL Patent: US 6541212-A 1 01-APR-2003;
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ACCESSION AR162849
VERSION AR162849.1 GI:16230194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 998)
AUTHORS Reiter,R.E. and Witte,O.N.
TITLE PSCA antibodies and hybridomas producing them
JOURNAL Patent: US 6258939-A 1 10-JUL-2001;
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 998)
AUTHORS Reiter,R.E. and Witte,O.N.
TITLE Methods for detecting prostate stem cell antigen protein
JOURNAL Patent: US 6541212-A 1 01-APR-2003;
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ACCESSION AX080304
VERSION AX080304.1 GI:13159773
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ORGANISM Homo sapiens
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REFERENCE
1. Reiter,R., Witte,O., Saffran,D.C. and Jakobovits,A.
PSCA: Prostate stem cell antigen and uses thereof
Patent: WO 0105427-A 1 25-JAN-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) ; Urogenesys, Inc.
(US)
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DB 250 AC 251

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DEFINITION Prostate stem cell antigen.
ACCESSION BD193367
VERSION BD193367.1 GI:33003106
KEYWORDS
SOURCE JP 2002511740-A/1.
ORGANISM unidentified
unclassified.
REFERENCE 1. (bases 1 to 998)
Reiter,R. and Witte,O.
Prostate stem cell antigen
Patent: JP 2002511740-A 1 16-APR-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
OS Unidentified
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PN JP 2002511740-A/1
PD 16-APR-2002
PF 10-MAR-1998 JP 1998539713
PR 10-MAR-1997 US 08/814279,12-JAN-1998 US 60/071141 PR
13-FEB-1998 US 60/074675
PI ROBERT REITER,OWEN WITTE
PC C07K7/08,C07K16/28,C12Q1/68,G01N33/53
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LOCUS
DEFINITION Sequence 23 from patent US 5856136.
ACCESSION AR026990
VERSION AR026990.1 GI:5937830
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1. (bases 1 to 288)
Au-Young,J.
AUTHORS
TITLE Human stem cell antigens
JOURNAL Patent: US 5856136-A 23 05-JAN-1999;
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Db 121 GAGAACTGCACCCAGCTGGGGAGAGAGTCTGGACCGCGCGCATCGGCGAGTTGGCCTC 180
QY 232 NTGACCGTATCAGCAAAA-GCTGCAGCTTGAATCGTGATGANTCAGGANTACTAC 290
Db 181 CTGACCGTATCAGCAAAAGGCTGCAGCTTGAATCGTGATGANTCAGGANTACTAC 240

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LOCUS AR026974 494 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5956136.
ACCESSION AR026974
VERSION AR026974.1 GI:5937814
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 494)
AUTHORS Au-Young, J.
TITLE Human stem cell antigens
JOURNAL Patent: US 5856136-A 4 05-JAN-1999;
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Best Local Similarity 98.3%; Pred. No. 3.9e-38;
Matches 236; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 52 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGAGCCAGGC 111
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RESULT 15
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DEFINITION Homo sapiens prostate stem cell antigen, mRNA (cDNA clone MGC:22972
IMAGE:4840974), complete cds.
ACCESSION BC023582
VERSION BC023582.2 GI:40225653
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1015)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.N., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Buffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
Strausberg, R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replaced gi:23958165.
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: ATCC/DCTP/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hri.nih.gov
Akter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,
Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 33 Row: m Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5031994.
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/tissue_type="Skin, melanotic melanoma, high MDR."
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/lab_host="DH10B-R"
/notes="Vector: pOTB7"
1. .1015
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Query Match      77.6%; Score 225; DB 9; Length 1015;
Best Local Similarity 98.3%; Pred. No. 3.5e-38;
Matches 236; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 52 GTGACCATGAAGGCTGTGCTGCTTGCCTCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 111
Db 1 GTGACCATGAAGGCTGTGCTGCTTGCCTCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60

QY 112 ACTGCCCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 171
Db 61 ACTGCCCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120

QY 172 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCCTC 231
Db 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCCTC 180

QY 232 NTGACCGTCATCAGCAAA-GCTGCAGCTTGAACTCGTGGATGANTCAGGANTACTAC 290
Db 181 CTGACCGTCATCAGCAAAAGGCTGCAGCTTGAACTCGTGGATGACTCAGGACTACTAC 240
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Search completed: September 18, 2004, 13:27:04
Job time : 1454.17 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:33:41 ; Search time 189,576 Seconds
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Title: US-09-079-874-1

Perfect score: 290

Sequence: 1 CATTGAGCCATATAAGT.....ATGANTCAGAGTACTAC 290

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
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- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	286	98.6	290	2	AAV80386 Nucleotid
2	286	98.6	290	2	AAV68603 Human PS1
3	275	94.8	1023	2	AAV80397 Consensus
4	275	94.8	1023	2	AAV68613 Human PS1
5	275	94.8	1023	2	AAV68614 Human PS1
6	275	94.8	1028	9	AD553926 Human pro
7	257.8	88.9	373	2	AAV40822 Human sec
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11	232.4	80.1	979	2	AAV36801 Human tra
12	227	78.3	279	2	AAV80388 Nucleotid
13	227	78.3	279	2	AAV68605 Human PS1
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20	225.4	77.7	998	3	AAV48374 Human pro
21	225	77.6	288	2	AAV38061 Human pro
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23	225	77.6	972	2	AAV80396 Nucleotid

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27	208	71.7	960	2	AAV52217	AAV52217
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29	208	71.7	960	4	AAV72375	AAV72375
30	208	71.7	960	6	ABK40257	ABK40257
31	208	71.7	960	7	ACA58909	ACA58909
32	208	71.7	960	7	ACA58306	ACA58306
33	208	71.7	960	7	ACA80013	ACA80013
34	208	71.7	960	7	ACD07413	ACD07413
35	208	71.7	960	7	ABX71461	ABX71461
36	208	71.7	960	7	ACH06793	ACH06793
37	208	71.7	960	7	ABX96030	ABX96030
38	208	71.7	960	7	ACA05351	ACA05351
39	208	71.7	960	7	ACD20018	ACD20018
40	208	71.7	960	7	ACA54821	ACA54821
41	208	71.7	960	8	ACD19656	ACD19656
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ALIGNMENTS

RESULT 1

AAV80386
ID AAV80386 standard; DNA; 290 BP.

XX
AC AAV80386;

XX
DT 23-FEB-1999 (first entry)

XX
DE Nucleotide sequence of Utl16 gene-specific clone 3353644.

XX
KW Utl16; urinary tract; epitope; antigen; detection; diagnosing;
monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
metastasis; ss.

XX
OS Homo sapiens.

XX
FN WO951824-A1.

XX
PD 19-NOV-1998.

XX
PF 15-MAY-1998; 98WO-US009972.

XX
PR 15-MAY-1997; 97US-00856652.

XX
PA (ABBO) ABBOTT LAB.

XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
Stroupe SD;

XX
DR WPI; 1999-045237/04.

XX
New method for detecting diseases of the urinary tract - comprises use of
a Utl16 polynucleotide, protein or antibodies, used for preventing and
treating urinary tract infections and cancer.

XX
Claim 1; Fig 1A-C; 113pp; English.

XX
Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
sequences of the Utl16 gene-specific clones derived from urinary tract
tissue. The invention relates to a method of detecting the presence of a
target Utl16 polynucleotide in a test sample using these Utl16-specific
sequences. Host cells transfected with an expression vector containing
the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
This polypeptide has at least one Utl16 epitope which can be used in a
method for detecting Utl16 antigen in a test sample. The polynucleotides

CC and polypeptides are useful for detecting, diagnosing, monitoring,
 CC staging, prognosticating, in vivo imaging, preventing, treating or
 CC determining the predisposition of a subject to diseases and conditions of
 CC the urinary tract, such as urinary tract cancer. Antibodies specifically
 CC binding to an epitope of Utl16 antigen, and agonists are useful for
 CC treating urinary tract diseases, tumours and metastases
 XX
 SQ Sequence 290 BP; 60 A; 89 C; 83 G; 54 T; 0 U; 4 Other;

Query Match 98.6%; Score 286; DB 2; Length 290;
 Best Local Similarity 100.0%; Pred. No. 6.2e-62;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DT 16-MAR-1999 (first entry)
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 KW Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 KW detection; therapy; prostate cancer; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9851805-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 15-MAY-1998; 98WO-US010041.
 XX
 PR 15-MAY-1997; 97US-00856653.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD;
 XX
 DR WPI; 1999-045234/04.
 XX
 PT New method for detecting diseases of the prostate - comprises use of a
 PT PS116 polynucleotide, protein or antibodies, useful for preventing and
 PT treating prostate infections and cancer.
 XX
 PS Claim 1; Page 91; 118pp; English.
 XX
 CC This sequence represents an expressed sequence tag (EST) clone of the
 CC PS116 gene isolated from a human prostate tissue library. This sequence

CC can be used in the method of the invention for detecting a target PS116
 CC polynucleotide (PN), that comprises: contacting a sample with at least 1
 CC PS116-specific PN or complement; and detecting the target PS116 PN where
 CC the specific PN has at least 50% identity with this sequence. The PNs,
 CC PS116 polypeptides or PS116 amplicons are used to detect prostate
 CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
 CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
 CC solid phase. The polypeptides are used for detecting PS116-specific Abs
 CC in a sample, and for producing Abs after immunising a subject. Plasmids
 CC encoding PS116 epitopes can also be administered to a subject to obtain
 CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
 CC staging, monitoring, prognosticating, in vivo imaging, preventing,
 CC treating or determining the predisposition of a subject to diseases and
 CC conditions of the prostate, such as prostate cancer. The Abs and agonists
 CC or inhibitors are useful for treating prostate diseases, tumours and
 CC metastases
 XX
 SQ Sequence 290 BP; 60 A; 89 C; 83 G; 54 T; 0 U; 4 Other;

Query Match 98.6%; Score 286; DB 2; Length 290;
 Best Local Similarity 100.0%; Pred. No. 6.2e-62;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATTGAGGCCATATAAAGTCACTGAGGNCCTTCCACACAGCCACCACTGACCATG 60
 Db 1 CATTGAGGCCATATAAAGTCACTGAGGNCCTTCCACACAGCCACCACTGACCATG 60
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 AC AAV80397;
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 DT 23-FEB-1999 (first entry)
 XX
 DE Consensus nucleotide sequence of Utl16 gene.
 XX
 KW Utl16; urinary tract; epitope; antigen; detection; diagnosing;
 KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
 KW metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 PN CDS 58..429
 FT /*tag= a
 FT /product= "Utl16 polypeptide"
 XX
 PN WO9851824-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 15-MAY-1998; 98WO-US009972.
 XX
 PR 15-MAY-1997; 97US-00856652.
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PA (ABBO ) ABBOTT LAB.
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
PI Stroupe SD;
XX WPI; 1999-045237/04.
DR P-PSDB; AAV86024.
XX
XX New method for detecting diseases of the urinary tract - comprises use of
PT a Utl16 polynucleotide, protein or antibodies, used for preventing and
PT treating urinary tract infections and cancer.
XX
XX Claim 1; Fig 1A-C; 113pp; English.
XX
XX This represents the consensus nucleotide sequence of the Utl16 gene. The
CC invention relates to a method of detecting the presence of a target Utl16
CC polynucleotide in a test sample using Utl16-specific sequences (AAV80386
CC to AAV80397). Host cells transfected with an expression vector containing
CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
CC This polypeptide has at least one Utl16 epitope which can be used in a
CC method for detecting Utl16 antigen in a test sample. The polynucleotides
CC and polypeptides are useful for detecting, diagnosing, monitoring,
CC staging, prognosticating, in vivo imaging, preventing, treating or
CC determining the predisposition of a subject to diseases and conditions of
CC the urinary tract, such as urinary tract cancer. Antibodies specifically
CC binding to an epitope of Utl16 antigen, and agonists are useful for
CC treating urinary tract diseases, tumours and metastases
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SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;
Query Match 94.8%; Score 275; DB 2; Length 1023;
Best Local Similarity 98.3%; Pred. No. 4.4e-59;
Matches 286; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 CATTGAGGCCATATAAGTCACCTGAGGCCTCTCCACCACAGCCACCAGTGACCATG 60
DB 1 CATTGAGGCCATATAAGTCACCTGAGGCCTCTCCACCACAGCCACCAGTGACCATG 60
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DB 61 AAGGCTGTCTGCTTGCCTTGTATGGCAGCTTGGCCCTGACGCCAGCTGCCCTG 120
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QY 181 ACCAGCTGGGAGCAGTGTGGACCGCGGCATCCGCGCATCTTGGCTCTNTGACCGTTC 240
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XX 16-MAR-1999 (first entry)
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XX Human PS116 EST clone 1543671H.
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XX Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
XX detection; therapy; prostate cancer; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO9851805-A1.
XX
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PD 19-NOV-1998.
XX
XX 15-MAY-1998; 98WO-US010041.
XX
XX 15-MAY-1997; 97US-00856653.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
XX WPI; 1999-045234/04.
XX
XX New method for detecting diseases of the prostate - comprises use of a
PT PS116 polynucleotide, protein or antibodies, useful for preventing and
PT treating prostate infections and cancer.
XX
XX Claim 1; Page 94; 118pp; English.
XX
XX This sequence represents an expressed sequence tag (EST) clone of the
CC PS116 gene isolated from a human prostate tissue library. This sequence
CC can be used in the method of the invention for detecting a target PS116
CC polynucleotide (PN), that comprises; contacting a sample with at least 1
CC PS116-specific PN or complement; and detecting the target PS116 PN, where
CC the specific PN has at least 50% identity with this sequence. The PNs,
CC PS116 polypeptides or PS116 amplicons are used to detect prostate
CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
CC solid phase. The polypeptides are used for detecting PS116-specific Abs
CC in a sample, and for producing Abs after immunising a subject. Plasmids
CC encoding PS116 epitopes can also be administered to a subject to obtain
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
CC treating or determining the predisposition of a subject to diseases and
CC conditions of the prostate, such as prostate cancer. The Abs and agonists
CC or inhibitors are useful for treating prostate diseases, tumours and
CC metastases
XX
SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;
Query Match 94.8%; Score 275; DB 2; Length 1023;
Best Local Similarity 98.3%; Pred. No. 4.4e-59;
Matches 286; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 CATTGAGGCCATATAAGTCACCTGAGGCCTCTCCACCACAGCCACCAGTGACCATG 60
DB 1 CATTGAGGCCATATAAGTCACCTGAGGCCTCTCCACCACAGCCACCAGTGACCATG 60
QY 61 AAGGCTGTCTGCTTGCCTTGTATGGCAGCTTGGCCCTGACGCCAGCTGCCCTG 120
DB 61 AAGGCTGTCTGCTTGCCTTGTATGGCAGCTTGGCCCTGACGCCAGCTGCCCTG 120
QY 121 CTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTGAGAACTGC 180
DB 121 CTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTGAGAACTGC 180
QY 181 ACCAGCTGGGAGCAGTGTGGACCGCGGCATCCGCGCATCTTGGCTCTNTGACCGTTC 240
DB 181 ACCAGCTGGGAGCAGTGTGGACCGCGGCATCCGCGCATCTTGGCTCTNTGACCGTTC 240
QY 241 ATCAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCAGGANTACTTAC 290
DB 241 ATCAGCAAAAGGCTGACGCTTGAACCTGCGTGGATGANTCAGGANTACTTAC 291
RESULT 5
AAV68614
ID AAV68614 standard; cDNA; 1023 BP.
XX
XX AAV68614;
AC
XX
XX 16-MAR-1999 (first entry)
DT
```

XX DE Human PS116 EST clone consensus sequence.

XX DE Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;

KW detection; therapy; prostate cancer; metastasis; ss.

XX OS Homo sapiens.

XX PN WO9851805-A1.

XX PD 19-NOV-1998.

XX PF 15-MAY-1998; 98WO-US010041.

XX PR 15-MAY-1997; 97US-00856653.

XX PS (ABSO) ABBOTT LAB.

XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;

PI Russell JC, Stroupe SD;

XX DR WPI; 1999-045234/04.

XX PT New method for detecting diseases of the prostate - comprises use of a

PT PS116 polynucleotide, protein or antibodies, useful for preventing and

PT treating prostate infections and cancer.

XX PS Claim 1; Page 94; 118pp; English.

XX CC This sequence represents an expressed sequence tag (EST) clone of the

CC PS116 gene isolated from a human prostate tissue library. This sequence

CC can be used in the method of the invention for detecting a target PS116

CC polynucleotide (PN), that comprises: contacting a sample with at least 1

CC PS116-specific PN or complement; and detecting the target PS116 PN, where

CC the specific PN has at least 50% identity with this sequence. The PNs,

CC PS116 polypeptides or PS116 amplicons are used to detect prostate

CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect

CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a

CC solid phase. The polypeptides are used for detecting PS116-specific Abs

CC in a sample, and for producing Abs after immunising a subject. Plasmids

CC encoding PS116 epitopes can also be administered to a subject to obtain

CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,

CC staging, monitoring, prognosticating, in vivo imaging, preventing,

CC treating or determining the predisposition of a subject to diseases and

CC conditions of the prostate, such as prostate cancer. The Abs and agonists

CC or inhibitors are useful for treating prostate diseases, tumours and

CC metastases

XX SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;

Query Match 94.8%; Score 275; DB 2; Length 1023;

Best Local Similarity 98.3%; Pred. No. 4.4e-59;

Matches 286; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CATTTCAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGAGTACCATTG 60

DB 1 CATTTCAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGAGTACCATTG 60

QY 61 AAGGCTGTGCTGTTGCCCTGTGATGGCAGGCTTGCCCTCGAGGCGGACTGCCCTG 120

DB 61 AAGGCTGTGCTGTTGCCCTGTGATGGCAGGCTTGCCCTCGAGGCGGACTGCCCTG 120

QY 121 CTGTGCTACTCTCTGCAAGCCAGGTGAGCAGAGGACTGCTGCAGGTGGAGACTGC 180

DB 121 CTGTGCTACTCTCTGCAAGCCAGGTGAGCAGAGGACTGCTGCAGGTGGAGACTGC 180

QY 181 ACCAGCTGGGGAGCAGTCTGACCCGCGCATCCGCGCGAGTTGGCTCTGACCGTTC 240

DB 181 ACCAGCTGGGGAGCAGTCTGACCCGCGCATCCGCGCGAGTTGGCTCTGACCGTTC 240

QY 241 ATCAGCAAA-GCTGCAGCTGACTCGGTGGATGANTCAGAGTACTACTAC 290

DB 241 ATCAGCAAAAGGCTGCGAGCTTGAAGTGGTGGATGACTCAGGACTACTAC 291

RESULT 6

AD853926

ID ADE53926 standard; cDNA; 1028 BP.

XX AC ADE53926;

XX AC ADE53926;

DT 29-JAN-2004 (first entry)

XX DE Human prostate cancer cDNA #273.

XX KW Human; prostate cancer; ss; cDNA combination; differential expression;

KW gene.

XX OS Homo sapiens.

XX PN US2003190640-A1.

XX PD 09-OCT-2003.

XX PF 29-MAY-2002; 2002US-00252157.

XX PR 31-MAY-2001; 2001US-0295048P.

XX PA (PARI/) FARIS M.

PA (PEAR/) PEARSON C I.

XX PI Faris M, Pearson CI;

XX WPI; 2003-831619/77.

XX PT New combination comprising cDNAs that are differentially expressed in

PT prostate cancer, useful for diagnosing, treating or monitoring the

PT progression of treatment of prostate cancer.

XX PS Claim 1; SEQ ID NO 273; 42pp; English.

XX CC The invention relates to a combination comprising a number of cDNAs

CC expressed in prostate cancer. The invention also relates to a method for

CC detecting differential expression of one or more cDNAs in a sample

CC containing nucleic acids by hybridising a substrate with the nucleic

CC acids, thus forming one or more hybridisation complexes, detecting

CC hybridisation complex formation and comparing the complexes formed with

CC standard complexes, where differences between the standard and the sample

CC complex formation indicate differential expression of cDNAs in the

CC sample. The differential expression is diagnostic of prostate cancer. The

CC invention also relates to proteins and antibodies related to the cDNAs.

CC The combination is useful for diagnosing, treating or monitoring the

CC progression of treatment of prostate cancer. The antibodies are useful

CC for detecting prostate cancer. This sequence represents a human prostate

CC cancer cDNA of the invention.

XX SQ Sequence 1028 BP; 199 A; 350 C; 288 G; 191 T; 0 U; 0 Other;

Query Match 94.8%; Score 275; DB 9; Length 1028;

Best Local Similarity 98.3%; Pred. No. 4.4e-59;

Matches 286; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CATTTCAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGAGTACCATTG 60

DB 1 CATTTCAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGAGTACCATTG 60

QY 61 AAGGCTGTGCTGTTGCCCTGTGATGGCAGGCTTGCCCTCGAGGCGGACTGCCCTG 120

DB 61 AAGGCTGTGCTGTTGCCCTGTGATGGCAGGCTTGCCCTCGAGGCGGACTGCCCTG 120

QY 121 CTGTGCTACTCTCTGCAAGCCAGGTGAGCAGAGGACTGCTGCAGGTGGAGACTGC 180

DB 121 CTGTGCTACTCTCTGCAAGCCAGGTGAGCAGAGGACTGCTGCAGGTGGAGACTGC 180

QY 181 ACCAGCTGGGGAGCAGTCTGACCCGCGCATCCGCGCGAGTTGGCTCTGACCGTTC 240

DB 181 ACCAGCTGGGGAGCAGTCTGACCCGCGCATCCGCGCGAGTTGGCTCTGACCGTTC 240

QY 241 ATCAGCAAA-GCTGCAGCTGACTCGGTGGATGANTCAGAGTACTACTAC 290

Db 181 ACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCCGCGAGTGGCCCTCCTGACCGTC 240
QY 241 ATCAGCAAA-GCTGAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 230
Db 241 ATCAGCAAGGCTGACAGTGTGAATGCGTGGATGACTCAGAGGACTACTAC 231
RESULT 7
ID AAX40622
AA 40622 standard; cDNA; 373 BP.
AC AAX40622;
XX
DT 18-JUN-1999 (first entry)
DE Human secreted protein 5' EST SEQ ID No: 222.
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
OS Homo sapiens.
XX
XX WO9906550-A2.
PN 11-FEB-1999.
XX
PD 31-JUL-1998; 98WO-IB001232.
PF
XX 01-AUG-1997; 97US-00905144.
PR
XX (GEST) GENSET.
PA
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
XX WPI: 1999-153780/13.
DR P-PSDB; AAY11900.
XX
PT New isolated prostate-derived nucleic acids - used to develop products
PT which may have cytokine, immune regulatory, haematopoiesis regulating,
PT anti-inflammatory or tumour inhibition activity.
XX
XX Claim 1; Page 346-347; 675pp; English.
XX
CC AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins expressed in prostate, and encode the proteins
CC given in AAY11716 to AAY11993 respectively. The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation and differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptides can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 373 BP; 75 A; 115 C; 108 G; 69 T; 0 U; 6 Other;
Query Match 88.9%; Score 257.8; DB 2; Length 373;
Best Local Similarity 95.5%; Pred. No. 7.1e-55;
Matches 278; Conservative 4; Mismatches 7; Indels 2; Gaps 2;
QY 1 CATTGGAGCCCATATAAGTACCTGAGGCNCTCTCCACACAGCCACCGAGTGACCATG 60

Db 54 CATTGGAGCCCATATAAA-NNACCTGAGGCCTCTCCACACAGCCACCGAGTGACCATG 112
QY 61 AAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTCCAGCCAGGCACTGCCCTG 120
Db 113 AAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTCCAGCCAGGCACTGCCCTG 172
QY 121 CTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGTGGAGAACTGC 180
Db 173 CTGTGCTACTCTCTGGARRGCCAGGTGRCACACGAGGACTGCTGCAGTGGAGAACTGC 232
QY 181 ACCAGCTGGGGAGCAGTGTGACCGCGGCATCCGCGCAGTGGCCCTCTGACCGTC 240
Db 233 ACCAGCTGGGGAGCAGTGTGACCGCGGCATCCGCGCAGTGGCCCTCTGACCGTC 292
QY 241 ATCAGCAAA-GCTGAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 290
Db 293 ATCAGCAAAAGGCTGACGTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 343
RESULT 8
AAC00612
ID AAC00612 standard; cDNA; 373 BP.
XX AAC00612;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 610.
DE
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EF1033401-A2.
PN
XX 06-SEP-2000.
PD
XX 21-FEB-2000; 2000EP-00200610.
PF
XX 26-FEB-1999; 99US-0122487P.
PR
XX (GEST) GENSET.
PA
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX WPI: 2000-500381/45.
DR P-PSDB; AAG00606.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 610; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 373 BP; 75 A; 115 C; 108 G; 69 T; 0 U; 6 Other;

Query Match 88.9%; Score 257.8; DB 3; Length 373;
 Best Local Similarity 95.5%; Pred. No. 7.1e-55;
 Matches 278; Conservative 4; Mismatches 7; Indels 2; Gaps 2;
 QY 1 CATTTGAGGCCATATAAAGTCACTTGAGGNCCTCTCCACACAGCCACCCAGTGACCATG 60
 Db 53 CATTTGAGGCCATATAA-NNACCTGAGGCCCTCTCCACACAGCCACCCAGTGACCATG 111
 QY 61 AAGCTGTGCTGCTGCCCTTGTATGTCAGGCTTGCCCTGAGCCAGGCACTGCCCTG 120
 Db 112 AAGCTGTGCTGCTGCCCTTGTATGTCAGGCTTGCCCTGAGCCAGGCACTGCCCTG 171
 QY 121 CTGTCTACTCTCTGAAAGCCAGGTGAGCAACAGGAGTGCCTGTCAGGTGGAGAACTGC 180
 Db 172 CTGTCTACTCTCTGARRGCCAGGTGAGCAACAGGAGTGCCTGTCAGGTGGAGAACTGC 231
 QY 181 ACCAGCTGGGGAGCATGTGTGACCGCGCGCATTCGCGGAGTGGCTCTGTCAGCCGTC 240
 Db 232 ACCAGCTGGGGAGCATGTGTGACCGCGCGCATTCGCGGAGTGGCTCTGTCAGCCGTC 291
 QY 241 ATCAGCAAA-GCTGAGCTTGAAGTCTGATGATGANTCAGAGGANTACTAC 290
 Db 292 ATCAGCAAAAGCTGAGCTTGAAGTCTGATGATGANTCAGAGGANTACTAC 342

RESULT 9
 AAV80387
 ID AAV80387 standard; DNA; 293 BP.
 XX AAV80387;
 DT 23-FEB-1999 (first entry)
 DE Nucleotide sequence of UT116 gene-specific clone 2804743.
 KW UT116; urinary tract; epitope; antigen; detection; diagnosing;
 KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
 KW metastasis; ss.
 OS Homo sapiens.
 PN WO9851824-A1.
 PD 19-NOV-1998.
 XX 15-MAY-1998; 98WO-US009972.
 XX 15-MAY-1997; 97US-00856652.
 PA (ABBO) ABBOTT LAB.
 XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
 PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
 PI Stroupe SD;
 DR WPI; 1999-045237/04.
 XX New method for detecting diseases of the urinary tract - comprises use of
 PT a UT116 polynucleotide, protein or antibodies, used for preventing and
 PT treating urinary tract infections and cancer.
 XX Claim 1; Fig 1A-C; 113pp; English.

Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
 CC sequences of the UT116 gene-specific clones derived from urinary tract
 CC tissue. The invention relates to a method of detecting the presence of a
 CC target UT116 polynucleotide in a test sample using these UT116-specific
 CC sequences. Host cells transfected with an expression vector containing
 CC the UT116 gene can be used to produce a UT116 polypeptide recombinantly.
 CC This polypeptide has at least one UT116 epitope which can be used in a
 CC method for detecting UT116 antigen in a test sample. The polynucleotides
 CC and polypeptides are useful for detecting, diagnosing, monitoring,
 CC staging, prognosticating, in vivo imaging, preventing, treating or

CC determining the predisposition of a subject to diseases and conditions of
 CC the urinary tract, such as urinary tract cancer. Antibodies specifically
 CC binding to an epitope of UT116 antigen, and agonists are useful for
 CC treating urinary tract diseases, tumours and metastases
 XX
 SQ Sequence 293 BP; 60 A; 92 C; 89 G; 52 T; 0 U; 0 Other;
 Query Match 86.2%; Score 250; DB 2; Length 293;
 Best Local Similarity 98.1%; Pred. No. 6e-53;
 Matches 261; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 26 GAGGNCCTCTCCACACAGCCACCCAGTGACCATGAGGCTGTGCTTGCCTGTGGA 85
 Db 1 GAGGNCCTCTCCACACAGCCACCCAGTGACCATGAGGCTGTGCTTGCCTGTGGA 60
 QY 86 TGGCAGGCTTGGCCCTGAGCCAGGCACTGCCCTGCTGTACTCTCTGCAAGCCAGG 145
 Db 61 TGGCAGGCTTGGCCCTGAGCCAGGCACTGCCCTGCTGTACTCTCTGCAAGCCAGG 120
 QY 146 TGAGCAACAGGAGCTGCTGTCAGGTGGAGAACTGCCAGCTGGGGAGGAGTGTGGA 205
 Db 121 TGAGCAACAGGAGCTGCTGTCAGGTGGAGAACTGCCAGCTGGGGAGGAGTGTGGA 180
 QY 206 CCGCGGCAATCCGCGAGTGGCCCTGTCAGGTCATCAGCAAA-GCTGCAAGCTGAACT 264
 Db 181 CCGCGGCAATCCGCGAGTGGCCCTGTCAGGTCATCAGCAAAAGGCTGCAAGCTGAACT 240
 QY 265 GCGTGGATGANTCAGAGGANTACTAC 290
 Db 241 GCGTGGATGANTCAGAGGANTACTAC 266

RESULT 10
 AAV68604
 ID AAV68604 standard; cDNA; 293 BP.
 XX AAV68604;
 AC AAV68604;
 DT 16-MAR-1999 (first entry)
 DE Human PS116 EST clone 2804743.
 XX Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 KW detection; therapy; prostate cancer; metastasis; ss.
 OS Homo sapiens.
 XX WO9851805-A1.
 PD 19-NOV-1998.
 XX 15-MAY-1998; 98WO-US010041.
 XX 15-MAY-1997; 97US-00856653.
 PA (ABBO) ABBOTT LAB.
 XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD;
 DR WPI; 1999-045234/04.
 XX New method for detecting diseases of the prostate - comprises use of a
 PT PS116 polynucleotide, protein or antibodies, useful for preventing and
 PT treating prostate infections and cancer.
 XX Claim 1; Page 91; 119pp; English.
 XX This sequence represents an expressed sequence tag (EST) clone of the
 CC PS116 gene isolated from a human prostate tissue library. This sequence
 CC can be used in the method of the invention for detecting a target PS116
 CC polynucleotide (PN), that comprises: contacting a sample with at least 1

CC PS116-specific PN or complement; and detecting the target PS116 PN, where
CC the specific PN has at least 50% identity with this sequence. The PNs,
CC PS116 polypeptides or PS116 amplicons are used to detect prostate
CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
CC solid phase. The polypeptides are used for detecting PS116-specific Abs
CC in a sample, and for producing Abs after immunising a subject. Plasmids
CC encoding PS116 epitopes can also be administered to a subject to obtain
CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC treating or determining the predisposition of a subject to diseases and
CC conditions of the prostate, such as prostate cancer. The Abs and agonists
CC or inhibitors are useful for treating prostate diseases, tumours and
CC metastases

XX:
SQ Sequence 293 BP; 60 A; 92 C; 89 G; 52 T; 0 U; 0 Other;

Query Match 86.2%; Score 250; DB 2; Length 293;
Best Local Similarity 98.1%; Pred. No. 6e-53;
Matches 261; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 26 GAGGNCCTCTCCACACAGCCACACAGTGCATGAGAGGCTGTGCTTCCCTGTGGA 85
DB 1 GAGGCCCTCTCCACACAGCCACACAGTGCATGAGAGGCTGTGCTTCCCTGTGGA 60
QY 86 TCGCAGGCTTGCCTCGAGCCAGGCACTGCCCTGCTGTACTCTCCGCAAGCCAGG 145
DB 61 TGCAGGCTTGCCTCGAGCCAGGCACTGCCCTGCTGTACTCTCCGCAAGCCAGG 120
QY 146 TGAGCAACGAGGACTGCTCGAGGTGGAGAACTGCACCCAGCTGGGGAGGAGTCTGGA 205
DB 121 TGAGCAACGAGGACTGCTCGAGGTGGAGAACTGCACCCAGCTGGGGAGGAGTCTGGA 180
QY 206 CGCGCGCATCCGCGAGTGGCCCTCTGACCGTCAATCAGCAAA-GCTGCAGCTGAACT 264
DB 181 CGCGCGCATCCGCGAGTGGCCCTCTGACCGTCAATCAGCAAAAGGCTGCACTTGAAC 240
QY 265 GCGTGGATGANTCAGAGGANTACTAC 290
DB 241 GCGTGGATGACTCAGAGACTACTAC 266

RESULT 11
AA36801
ID AA36801 standard; DNA; 979 BP.
XX
AC AA36801;

XX 14-JUL-1999 (first entry)
XX Human transmembrane protein coding sequence, HP01244.
XX Transmembrane protein; human; cell membrane; proliferation; diagnosis;
XX cell differentiation; carcinostatic agent; probe; gene therapy;
XX signal transduction; apoptosis; inhibitor;
XX phosphatidylethanolamine N-methyltransferase; ss.

XX Homo sapiens.
XX WO9918203-A2.
XX
XX 15-APR-1999.
XX 05-OCT-1998; 98WO-UP004475.
XX
XX 08-OCT-1997; 97JP-00276271.
XX
XX (SAGA) SAGAMI CHEM RES CENT.
XX (PROT-) PROTEGENE INC.

XX Kato S, Yamaguchi T, Sekine S, Kobayashi M;
XX WPI; 1999-277268/23.

DR P-PSDB; AAY13938.
XX Human transmembrane proteins and nucleotide sequences.
PT
XX Claim 4; Page 104-105; 139pp; English.

XX This sequence encodes a human transmembrane protein of the invention. All
CC of the proteins exist in the cell membrane, so are considered to be
CC proteins controlling the proliferation and differentiation of the cells.
CC They may be useful as carcinostatic agents or as antigens for preparing
CC antibodies against the proteins. The cDNAs can be used as probes for gene
CC diagnosis and gene sources for gene therapy, as well as for large-scale
CC expression of the proteins. The HP01498 (see AAY13939) protein may be
CC associated with signal transduction associated with apoptosis, and
CC therefore useful in inhibition of apoptosis. The HP01962 (see AAY13943)
CC protein can be used to treat diseases associated with
CC phosphatidylethanolamine N-methyltransferase. The proteins are identified
CC by the presence of a hydrophobic transmembrane region, knowledge of the
CC protein function is not required, as in e.g. methods of expression
CC cloning

SQ Sequence 979 BP; 183 A; 334 C; 280 G; 182 T; 0 U; 0 Other;

Query Match 80.1%; Score 232.4; DB 2; Length 979;
Best Local Similarity 98.0%; Pred. No. 1.9e-48;
Matches 244; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 43 AGCCACCACTGACCATGAGGCTGTGCTTCCCTGTGATGCGAGGCTTGGCCCTG 102
DB 1 AGCCACCACTGACCATGAGGCTGTGCTTCCCTGTGATGCGAGGCTTGGCCCTG 60
QY 103 CAGCCAGGCACTGCCCTGTGTCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 162
DB 61 CAGCCAGGCACTGCCCTGTGTCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 120
QY 163 CTGAGGTGAGAACTGCACCCAGCTGGGGAGGAGTGTGGACCGCGCATCCGGCA 222
DB 121 CTGAGGTGAGAACTGCACCCAGCTGGGGAGGAGTGTGGACCGCGCATCCGGCA 180
QY 223 GTTGGCTCTNTGACCGTCATCAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCAG 281
DB 181 GTTGGCTCTCTGACCGTCATCAGCAAAAGGCTGAGCTTGAACCTGCGTGGATGANTCAG 240
QY 282 GANTACTAC 290
DB 241 GACTACTAC 249

RESULT 12
AAV80388
ID AAV80388 standard; DNA; 279 BP.
XX
AC AAV80388;
XX
XX 23-FEB-1999 (first entry)

XX Nucleotide sequence of UT116 gene-specific clone 1891065.
XX UT116; urinary tract; epitope; antigen; detection; diagnosing;
XX monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
XX metastasis; ss.

XX Homo sapiens.
XX WO9851824-A1.
XX
XX 19-NOV-1998.
XX 15-MAY-1998; 98WO-US009972.
XX
XX 15-MAY-1997; 97US-00856652.
XX
XX (ABBO) ABBOTT LAB.

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XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
PI Stroupe SD;
XX WPI; 1999-045237/04.
XX
XX PT New method for detecting diseases of the urinary tract - comprises use of
PT a Utl16 polynucleotide, protein or antibodies, used for preventing and
PT treating urinary tract infections and cancer.
XX
XX Claim 1; Fig 1A-C; 113pp; English.
XX
XX CC Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
CC sequences of the Utl16 gene-specific clones derived from urinary tract
CC tissue. The invention relates to a method of detecting the presence of a
CC target Utl16 polynucleotide in a test sample using these Utl16-specific
CC sequences. Host cells transfected with an expression vector containing
CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
CC This polypeptide has at least one Utl16 epitope which can be used in a
CC method for detecting Utl16 antigen in a test sample. The polynucleotides
CC and polypeptides are useful for detecting, diagnosing, monitoring,
CC staging, prognosticating, in vivo imaging, preventing, treating or
CC determining the predisposition of a subject to diseases and conditions of
CC the urinary tract, such as urinary tract cancer. Antibodies specifically
CC binding to an epitope of Utl16 antigen, and agonists are useful for
CC treating urinary tract diseases, tumours and metastases
XX
XX SQ Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;
Query Match 78.3%; Score 227; DB 2; Length 279;
Best Local Similarity 98.3%; Pred. No. 3.2e-47;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGCCCTGCAGCCAG 109
Db 1 CAGTGACCATGAAGCTGTGCTGCTTGTGATGGCAGGCTTGCCCTGCAGCCAG 60
QY 110 GCAGTGCCTGCTGTGCTTACTCTCTGAAAGCCAGGTGAGCAACGAGACTGCTGCAGG 169
Db 61 GCAGTGCCTGCTGTGCTTACTCTCTGAAAGCCAGGTGAGCAACGAGACTGCTGCAGG 120
QY 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGCATCCGCGAGTTGCC 229
Db 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGCATCCGCGAGTTGCC 180
QY 230 TCNTGACCGTTCATCAGCAA-GCTGCAGCTTGAAGTGGGTGGATGANTCAGAGGACT 288
Db 181 TCCTGACCGTTCATCAGCAAAGGCTGCAGTTGAAGTGGGTGGATGANTCAGAGGACT 240
QY 289 AC 290
Db 241 AC 242
RESULT 13
AAV68605
ID AAV68605 standard; cDNA; 279 BP.
XX
XX AC AAV68605;
XX
XX DT 16-MAR-1999 (first entry)
XX
XX DE Human PS116 EST clone 1891065.
XX
XX KW Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
XX detection; therapy; prostate cancer; metastasis; ss.
XX
XX OS Homo sapiens.
XX
XX PN W09851805-A1.
XX
XX DT 19-NOV-1998.
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XX PF 15-MAY-1998; 98WO-US010041.
XX PR 15-MAY-1997; 97US-00856653.
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX WPI; 1999-045234/04.
XX
XX PT New method for detecting diseases of the prostate - comprises use of a
PT PS116 polynucleotide, protein or antibodies, useful for preventing and
PT treating prostate infections and cancer.
XX
XX Claim 1; Page 92; 118pp; English.
XX
XX CC This sequence represents an expressed sequence tag (EST) clone of the
CC PS116 gene isolated from a human prostate tissue library. This sequence
CC can be used in the method of the invention for detecting a target PS116
CC polynucleotide (PN), that comprises: contacting a sample with at least 1
CC PS116-specific PN or complement; and detecting the target PS116 PN, where
CC the specific PN has at least 50% identity with this sequence. The PNs,
CC PS116 polypeptides or PS116 amplicons are used to detect prostate
CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
CC solid phase. The polypeptides are used for detecting PS116-specific Abs
CC in a sample, and for producing Abs after immunising a subject. Plasmids
CC encoding PS116 epitopes can also be administered to a subject to obtain
CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC treating or determining the predisposition of a subject to diseases and
CC conditions of the prostate, such as prostate cancer. The Abs and agonists
CC or inhibitors are useful for treating prostate diseases, tumours and
XX
XX SQ Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;
Query Match 78.3%; Score 227; DB 2; Length 279;
Best Local Similarity 98.3%; Pred. No. 3.2e-47;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGCCCTGCAGCCAG 109
Db 1 CAGTGACCATGAAGCTGTGCTGCTTGTGATGGCAGGCTTGCCCTGCAGCCAG 60
QY 110 GCAGTGCCTGCTGTGCTTACTCTCTGAAAGCCAGGTGAGCAACGAGACTGCTGCAGG 169
Db 61 GCAGTGCCTGCTGTGCTTACTCTCTGAAAGCCAGGTGAGCAACGAGACTGCTGCAGG 120
QY 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGCATCCGCGAGTTGCC 229
Db 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGCATCCGCGAGTTGCC 180
QY 230 TCNTGACCGTTCATCAGCAA-GCTGCAGCTTGAAGTGGGTGGATGANTCAGAGGACT 288
Db 181 TCCTGACCGTTCATCAGCAAAGGCTGCAGTTGAAGTGGGTGGATGANTCAGAGGACT 240
QY 289 AC 290
Db 241 AC 242
RESULT 14
ACG51040
ID ACC51040 standard; cDNA; 990 BP.
XX
XX AC ACC51040;
XX
XX DT 12-JUN-2003 (first entry)
XX
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QY 230 TCNTGACCGTCATCAGCAAA-GCTGCAGCTTGAACTGGTGATGANTCAGGANTACT 288
Db 190 TCCTGACCGTCATCAGCAAAAGGCTGCAGCTTGAACTGGTGATGANTCAGGANTACT 249

QY 289 AC 290
Db 250 AC 251

Search completed: September 18, 2004, 07:06:54
Job time : 194.576 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: September 18, 2004, 06:05:35 ; Search time 33.8779 Seconds
(without alignments)
4750.463 Million cell updates/sec

Title: US-09-079-874-1
Perfect score: 290
Sequence: 1 CATTTGAGGCATATAAGT.....ATGANTCAGGANTACTAC 290

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/6C_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	78.3	998	3	US-09-203-939-1
2	227	78.3	998	3	US-09-251-835-1
3	227	78.3	998	3	US-09-318-503-1
4	227	78.3	998	3	US-09-038-261A-1
5	227	78.3	998	4	US-09-564-329A-1
6	225	77.6	494	2	US-08-675-508-23
7	225	77.6	494	2	US-08-675-508-4
8	214.4	73.9	232	2	US-08-675-508-25
9	208	71.7	960	4	US-09-907-794A-17
10	208	71.7	960	4	US-09-905-125A-17
11	208	71.7	960	4	US-09-902-775A-17
12	176	60.7	286	2	US-08-675-508-21
13	107.6	37.1	441	3	US-09-203-939-3
14	107.6	37.1	441	3	US-09-251-835-3
15	107.6	37.1	441	3	US-09-318-503-3
16	107.6	37.1	441	3	US-09-038-261A-3
17	107.6	37.1	441	4	US-09-564-329A-3
18	52.4	18.1	280	2	US-08-675-508-17
19	52.2	18.0	262	2	US-08-675-508-10
20	52.2	18.0	289	2	US-08-675-508-11
21	52.2	18.0	537	2	US-08-675-508-3
22	52.2	18.0	1066	1	US-08-154-916-1
23	52.2	18.0	1095	1	US-09-139-424-1
24	52.2	18.0	1163	3	US-08-746-397-1
25	51.2	17.7	266	2	US-08-675-508-16
26	51.2	17.7	335	2	US-08-675-508-12
27	46.8	16.1	196	2	US-08-675-508-8

28	44.4	15.3	275	2	US-08-675-508-18	Sequence 18, Appl
29	44	15.2	44	4	US-09-907-794A-21	Sequence 21, Appl
30	44	15.2	44	4	US-09-905-125A-21	Sequence 21, Appl
31	44	15.2	44	4	US-09-902-775A-21	Sequence 21, Appl
32	42.6	14.7	261	2	US-08-675-508-13	Sequence 13, Appl
33	41	14.1	1491	4	US-09-252-991A-9935	Sequence 9935, Ap
34	41	14.1	1656	4	US-09-252-991A-9845	Sequence 9845, Ap
35	41	14.1	2007	4	US-09-252-991A-10141	Sequence 10141, A
36	39.2	13.5	5184	4	US-09-561-709B-4	Sequence 4, Appl
37	39.2	13.5	5184	4	US-09-252-991A-908	Sequence 908, App
38	38.8	13.4	903	4	US-09-252-991A-1128	Sequence 1128, Ap
39	38.8	13.4	1551	4	US-09-620-312D-30	Sequence 30, Appl
40	36.6	12.6	3650	2	US-08-675-508-15	Sequence 15, Appl
41	36.2	12.5	294	2	US-09-252-991A-4051	Sequence 4051, Ap
42	36	12.4	492	4	US-09-252-991A-3983	Sequence 3983, Ap
43	36	12.4	1077	4	US-09-252-991A-3896	Sequence 3896, Ap
44	36	12.4	1278	4	US-09-252-991A-3924	Sequence 3924, Ap
45	36	12.4	1977	4	US-09-252-991A-3924	Sequence 3924, Ap

ALIGNMENTS

RESULT 1

US-09-203-939-1
; Sequence 1, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435-54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)

NAME/KEY: misc_feature
LOCATION: (646)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (697)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (926)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
US-09-203-939-1

Query Match 78.3%; Score 227; DB 3; Length 998;

Best Local Similarity 98.3%; Pred. No. 2.2e-52;

Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 50 CAGTGACCATGAAGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 109

Db 10 CAGTGACCATGAAGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 69

QY 110 GCATGCGCCTGTGCTGTACTCTCTCAAGCCAGGTGAGCAAGGACTGCTGCAGG 169

Db 70 GCATGCGCCTGTGCTGTACTCTCTCAAGCCAGGTGAGCAAGGACTGCTGCAGG 129

QY 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCATCCGGCAGTTGGCC 229

Db 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCATCCGGCAGTTGGCC 189

QY 230 TCNTGACCGTCATCAGCAAA-GCTGCAGCTTGAAGTGGTGGATGANTCAGAGANTACT 288

Db 190 TCCTGACCGTCATCAGCAAAAGCTGCAGCTTGAAGTGGTGGATGANTCAGAGANTACT 249

QY 289 AC 290

Db 250 AC 251

RESULT 2

US-09-251-835-1

Sequence 1, Application US/09251835A

Patent No. 6261789

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN

FILE REFERENCE: 30435.54US12

CURRENT APPLICATION NUMBER: US/09/251,835A

CURRENT FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 08/814,279

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: 60/074,675

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 09/038,261

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 09/203,939

PRIOR FILING DATE: 1998-12-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 998

TYPE: DNA

ORGANISM: HUMAN PSCA (hPSCA)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (543)

OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (580)

OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (584)

OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)

NAME/KEY: misc_feature
LOCATION: (604)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (608)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (615)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (636)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (640)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (646)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (697)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc_feature
LOCATION: (926)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
US-09-251-835-1

Query Match 78.3%; Score 227; DB 3; Length 998;

Best Local Similarity 98.3%; Pred. No. 2.2e-52;

Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 50 CAGTGACCATGAAGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 109

Db 10 CAGTGACCATGAAGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 69

QY 110 GCATGCGCCTGTGCTGTACTCTCTCAAGCCAGGTGAGCAAGGACTGCTGCAGG 169

Db 70 GCATGCGCCTGTGCTGTACTCTCTCAAGCCAGGTGAGCAAGGACTGCTGCAGG 129

QY 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCATCCGGCAGTTGGCC 229

Db 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCATCCGGCAGTTGGCC 189

QY 230 TCNTGACCGTCATCAGCAAA-GCTGCAGCTTGAAGTGGTGGATGANTCAGAGANTACT 288

Db 190 TCCTGACCGTCATCAGCAAAAGCTGCAGCTTGAAGTGGTGGATGANTCAGAGANTACT 249

QY 289 AC 290

Db 250 AC 251

RESULT 3

US-09-318-503-1

Sequence 1, Application US/09318503A

Patent No. 6261791

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF.

FILE REFERENCE: 30435.54US13

CURRENT APPLICATION NUMBER: US/09/318,503A

CURRENT FILING DATE: 1999-05-25

EARLIER APPLICATION NUMBER: 08/814,279

EARLIER FILING DATE: 1997-03-10

EARLIER APPLICATION NUMBER: 60/071,141

EARLIER FILING DATE: 1998-01-12

EARLIER APPLICATION NUMBER: 60/074,675

EARLIER FILING DATE: 1998-02-13

EARLIER APPLICATION NUMBER: 09/038,261

EARLIER FILING DATE: 1998-03-10

EARLIER APPLICATION NUMBER: 09/203,939

EARLIER FILING DATE: 1998-12-02

EARLIER APPLICATION NUMBER: 09/251,835

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 QY 230 TCNTGACCGTCAATCAGCAAA-GCTGACGCTTCAACTGCGTGGATGANTCAGAGGACTACT 288
 Db 190 TCCTGACCGTCAATCAGCAAAAGCTGACCTTGAACCTGGTGGATGACTCAGAGGACTACT 249
 QY 289 AC 290
 Db 250 AC 251

RESULT 5

US-09-564-329A-1
 ; Sequence 1, Application US/09564329A
 ; Patent No. 6541212
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/09/564,329A
 ; PRIORITY FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 09/308,503
 ; PRIOR FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 998
 ; TYPE: DNA
 ; ORGANISM: HUMAN PSCA (hPSCA)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (543)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; NAME/KEY: misc_feature
 ; LOCATION: (580)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; NAME/KEY: misc_feature
 ; LOCATION: (584)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; NAME/KEY: misc_feature
 ; LOCATION: (604)
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 ; NAME/KEY: misc_feature

; LOCATION: (615)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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 ; NAME/KEY: misc_feature
 ; LOCATION: (640)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; NAME/KEY: misc_feature
 ; LOCATION: (646)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; NAME/KEY: misc_feature
 ; LOCATION: (697)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; NAME/KEY: misc_feature
 ; LOCATION: (926)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; LOCATION: (926)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 ; US-09-564-329A-1

Query Match 78.3%; Score 227; DB 4; Length 998;

Best Local Similarity 98.3%; Pred. No. 2.2e-52;

Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 50 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTGATGCGCAGGCTTGGCCCTGCAGCCAG 109
 Db 10 CAGTGACCATGAAGCTGTGCTGCTTGTGATGCGCAGGCTTGGCCCTGCAGCCAG 69
 QY 110 GCACTGCCCTGTGTGCTACTTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCTGCGAGG 169
 Db 70 GCACTGCCCTGTGTGCTACTTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCTGCGAGG 129
 QY 170 TGGAGAATGCAACCCAGCTGGGGAGCAGTGTGACCGCGCGCATCGGCGAGTTGSCC 229
 Db 130 TGGAGAATGCAACCCAGCTGGGGAGCAGTGTGACCGCGCGCATCGGCGAGTTGSCC 189
 QY 230 TCNTGACCGTCAATCAGCAAA-GCTGACGCTTGAACCTGGTGGATGANTCAGAGGACTACT 288
 Db 190 TCCTGACCGTCAATCAGCAAAAGCTGACCTTGAACCTGGTGGATGACTCAGAGGACTACT 249
 QY 289 AC 290
 Db 250 AC 251

RESULT 6

US-08-675-508-23
 ; Sequence 23, Application US/08675508
 ; Patent No. 5856136
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/675,508
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0066 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
IMMEDIATE SOURCE:
LIBRARY: BLADTUT02
CLONE: 1312529
US-08-675-508-23

Query Match 77.6%; Score 225; DB 2; Length 288;
Best Local Similarity 98.3%; Pred. No. 5.4e-52;
Matches 236; Conservative 0; Mismatches 3; Indels 1; Gaps 1

QY 52 GTGACCATGAAGGCTGTGCTGCTTGCCTCTTTGATGCGAGGCTTGCCCTCGAGCCAGGC 111
DB 1 GTGACCATGAAGGCTGTGCTGCTTGCCTCTTTGATGCGAGGCTTGCCCTCGAGCCAGGC 60
QY 112 ACTGCGCTGCTGTGCTACTCTCTGAAGCCCGAGTGAAGCAACGAGGACTGCTCTGCAGGTG 171
DB 61 ACTGCGCTGCTGTGCTACTCTCTGAAGCCCGAGTGAAGCAACGAGGACTGCTCTGCAGGTG 120
QY 172 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCCTC 231
DB 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCCTC 180
QY 232 NTGACCGTCATCAGCAAA-GCTGCAGCTTGAAGCTGCGTGTGATCAAGANTACTATC 290
DB 181 CTGACCGTCATCAGCAAAAGGCTGACGTTGAAGCTGCGTGTGATCAAGANTACTATC 240

RESULT 7
US-08-675-508-4
Sequence 4, Application US/08675508
Patent No. 5856136
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0066 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
IMMEDIATE SOURCE:
LIBRARY: SCAH-2

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DB	61	CTGCCCTGCTGTGCTACTCTCTCAAGCCCAAGGTGAGCAACGAGGACTGCCTCAGGTGG	120
QY	173	AGAACTGCACCCAGCTGGGGGAGCAGTCTCGACCGCGGCATCTCCGGCAGTTGGCCTCN	232
DB	121	AGAACTGCACCCAGCTGGGGGAGCAGTCTCGACCGCGGCATCTCCGGCAGTTGGCCTCC	180
QY	233	TGACCGTCAATCAGCAA--GCTGCAGCTTGAACTGCCTGGATGANTCACAGG	282
DB	181	TGACCGTCAATCAACAAAGGGTTGAGCTTGAACTGCCTGGATGACTCACAGG	232

RESULT 9
US-09-907-794A-17
; Sequence 17, Application US/09907794A

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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-794A-17

Query Match          71.7%; Score 208; DB 4; Length 960;
Best Local Similarity 98.2%; Pred. No. 2,9e-47;
Matches 219; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      69  GCTGCTTGCCTTTGATGGCAGGCTTGCCCTTGCAGCCAGGCACTGCCCTGTGTGCTA 128
Db      1  GCTGCTTGCCTTTGATGGCAGGCTTGCCCTTGCAGCCAGGCACTGCCCTGTGTGCTA 60

Qy      129 CTCCTGCAAGCCCGGTGAGCAACGAGGACTCCCTTGCAGGTGGAACTGCACCCAGCT 188
Db      61  CTCCTGCAAGCCCGGTGAGCAACGAGGACTCCCTTGCAGGTGGAACTGCACCCAGCT 120

Qy      189 GGGGGAGCAGTGTGGACCCGCGCCATCCGCGCAGTTGGCTCMTGACCGTCATCAGCAA 248
Db      121 GGGGGAGCAGTGTGGACCCGCGCGCATCCGCGCAGTTGGCTCCTGACCGTCATCAGCAA 180

Qy      249 A-GCTCAGCTTGAACCTGGTGATGANTCACAGGANTACTAC 290
Db      181 AGCTCAGCTTGAACCTGGTGATGACTCACAGGACTACTAC 223

```

RESULT 10
US-09-905-125A-17
: Sequence 17, Application US/09905125A

PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 17
LENGTH: 960
TYPE: DNA
ORGANISM: Homo sapiens
US-09-905-125A-17

Query Match 71.7%; Score 208; DB 4; Length 960;
Best Local Similarity 98.2%; Pred. No. 2.9e-47;
Matches 219; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 69 GCTGTTGCCCTTGTATGCGAGGCTTGGCCCTGCGAGCCAGGCACTGCGCTGTGCTA 128
DB 1 GCTGTTGCCCTTGTATGCGAGGCTTGGCCCTGCGAGCCAGGCACTGCGCTGTGCTA 60
QY 129 CTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGAGGTGAGAACTGCACCCAGCT 188
DB 61 CTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGAGGTGAGAACTGCACCCAGCT 120
QY 189 GGGGAGCAGTCTGAGCCGCGGATCGGCGAGTTCGCTGAGGTGAGAACTGCACCCAGCT 248
DB 121 GGGGAGCAGTCTGAGCCGCGGATCGGCGAGTTCGCTGAGGTGAGAACTGCACCCAGCT 180
QY 249 A-GCTGCACTTGAATGCTGCTGAGTTCAGGAGTTCAGGAGTACTAC 290
DB 181 AGGCTGCACTTGAATGCTGCTGAGTTCAGGAGTACTAC 223

RESULT 11
US-09-902-775A-17
Sequence 17, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 17
LENGTH: 960
TYPE: DNA
ORGANISM: Homo sapiens
US-09-902-775A-17

Query Match 71.7%; Score 208; DB 4; Length 960;
Best Local Similarity 98.2%; Pred. No. 2.9e-47;
Matches 219; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 69 GCTGTTGCCCTTGTATGCGAGGCTTGGCCCTGCGAGCCAGGCACTGCGCTGTGCTA 128
DB 1 GCTGTTGCCCTTGTATGCGAGGCTTGGCCCTGCGAGCCAGGCACTGCGCTGTGCTA 60

Blank Sheet

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 06:17:58 ; Search time 217.341 Seconds
(without alignments)
6734.858 Million cell updates/sec

Title: US-09-079-874-1

Perfect score: 290

Sequence: 1 CATTGAGCCATATAAAGT.....ATGANTCAGCAGTACTAC 290

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match.100%

Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	286	98.6	290	11	US-09-080-140-1
2	275	94.8	1023	11	US-09-080-140-11
3	275	94.8	1023	11	US-09-080-140-12
4	275	94.8	1028	11	US-10-252-157-273
5	250	86.2	293	11	US-09-080-140-2
6	227	78.3	279	11	US-09-080-140-3
7	227	78.3	990	13	US-10-240-425-386
8	227	78.3	990	16	US-10-117-937-87
9	227	78.3	998	17	US-10-188-832-168
10	227	78.3	998	9	US-09-564-329A-1
11	227	78.3	998	9	US-09-855-153-1
12	227	78.3	998	9	US-09-854-811-1
13	227	78.3	998	9	US-09-934-773-1
14	227	78.3	998	9	US-09-963-620-1

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15 227 78.3 998 10 US-09-855-632-1 Sequence 1, Appli
16 227 78.3 998 15 US-10-225-784-1 Sequence 1, Appli
17 227 78.3 998 15 US-10-224-720-1 Sequence 1, Appli
18 227 78.3 998 15 US-10-225-779-1 Sequence 1, Appli
19 227 78.3 998 16 US-10-374-381-1 Sequence 1, Appli
20 227 78.3 998 16 US-10-446-542-1 Sequence 1, Appli
21 225 77.6 288 9 US-09-334-586A-23 Sequence 23, Appli
22 225 77.6 494 9 US-09-934-586A-4 Sequence 4, Appli
23 214.4 73.9 232 9 US-09-334-586A-25 Sequence 25, Appli
24 208 71.7 960 9 US-09-909-320-17 Sequence 17, Appli
25 208 71.7 960 9 US-09-905-088B-17 Sequence 17, Appli
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29 208 71.7 960 9 US-09-907-841-17 Sequence 17, Appli
30 208 71.7 960 10 US-09-904-011-17 Sequence 17, Appli
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32 208 71.7 960 10 US-09-906-838-17 Sequence 17, Appli
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39 208 71.7 960 10 US-09-906-646-17 Sequence 17, Appli
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42 208 71.7 960 10 US-09-902-903-17 Sequence 17, Appli
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ALIGNMENTS

RESULT 1

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US-09-080-140-1
; Sequence 1, Application US/09080140
; Publication No. US20040018553A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,140
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: 08/856,653
 FILING DATE: 15-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6105.US.P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEFAX: 847/938-2623
 TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 290 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: base_polymorphism
 LOCATION: 31
 OTHER INFORMATION: /note= " N' represents an A or G or
 OTHER INFORMATION: T or C polymorphism at this position"

FEATURE:
 NAME/KEY: base_polymorphism

LOCATION: 232
 OTHER INFORMATION: /note= " N' represents an A or G or
 OTHER INFORMATION: T or C polymorphism at this position"

FEATURE:
 NAME/KEY: base_polymorphism

LOCATION: 275
 OTHER INFORMATION: /note= " N' represents an A or G or
 OTHER INFORMATION: T or C polymorphism at this position"

FEATURE:
 NAME/KEY: base_polymorphism

LOCATION: 284
 OTHER INFORMATION: /note= " N' represents an A or G or
 OTHER INFORMATION: T or C polymorphism at this position"

US-09-080-140-1

Query Match 98.6%; Score 286; DB 11; Length 290;
 Best Local Similarity 100.0%; Pred. No. 4.8e-78;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CATTGAGGCCATATAAGTCACTGAGGCNCTCTCCACACAGCCACCCAGTGACCATG	60
DB	1	CATTGAGGCCATATAAGTCACTGAGGCNCTCTCCACACAGCCACCCAGTGACCATG	60
QY	61	AAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTGCGAGGCACTGCCCTG	120
DB	61	AAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTGCGAGGCACTGCCCTG	120
QY	121	CTGTGCTACTCTCTGAAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTGGAGACTGC	180
DB	121	CTGTGCTACTCTCTGAAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTGGAGACTGC	180
QY	181	ACCCAGCTGGGAGAGAGTGGACCGCGCATCCGCGAGTTGGCTCTNTGACCGTC	240
DB	181	ACCCAGCTGGGAGAGAGTGGACCGCGCATCCGCGAGTTGGCTCTNTGACCGTC	240
QY	241	ATCAGCAAAAGCTGCAGCTTGAATCGGTGGATGANTCAGGANTACTAC	290
DB	241	ATCAGCAAAAGCTGCAGCTTGAATCGGTGGATGANTCAGGANTACTAC	290

RESULT 2

US-09-080-140-11

Sequence 11, Application US/09080140
 Publication No. US20040018553A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

APPLICANT: COHEN MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GORDON, JULIAN

APPLICANT: GRANADOS, EDWARD N.
 APPLICANT: HODGES, STEVEN C.
 APPLICANT: KLASS, MICHAEL R.
 APPLICANT: KRATOCHVIL, JON D.
 APPLICANT: ROBERTS-RAPP, LISA
 APPLICANT: RUSSELL, JOHN C.
 APPLICANT: STROUPE, STEPHEN D.
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/080,140
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/856,653
 FILING DATE: 15-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6105.US.P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEFAX: 847/938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1023 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-080-140-11

QY	1	CATTGAGGCCATATAAGTCACTGAGGCNCTCTCCACACAGCCACCCAGTGACCATG	60
DB	1	CATTGAGGCCATATAAGTCACTGAGGCNCTCTCCACACAGCCACCCAGTGACCATG	60
QY	61	AAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTGCGAGGCACTGCCCTG	120
DB	61	AAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTGCGAGGCACTGCCCTG	120
QY	121	CTGTGCTACTCTCTGAAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTGGAGACTGC	180
DB	121	CTGTGCTACTCTCTGAAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTGGAGACTGC	180
QY	181	ACCCAGCTGGGAGAGAGTGGACCGCGCATCCGCGAGTTGGCTCTNTGACCGTC	240
DB	181	ACCCAGCTGGGAGAGAGTGGACCGCGCATCCGCGAGTTGGCTCTNTGACCGTC	240
QY	241	ATCAGCAAAAGCTGCAGCTTGAATCGGTGGATGANTCAGGANTACTAC	290
DB	241	ATCAGCAAAAGCTGCAGCTTGAATCGGTGGATGANTCAGGANTACTAC	291

RESULT 3

US-09-080-140-12

; Sequence 12, Application US/09080140

Publication No. US20040018553A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080.140
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856.653
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6105.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-080-140-12

Query Match 94.8%; Score 275; DB 11; Length 1023;
Best Local Similarity 98.3%; Pred. No. 1.3e-74;
Matches 286; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 CATTGAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCGACCCAGTGCACCATG 60
Db 1 CATTGAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCGACCCAGTGCACCATG 60
QY 61 AAGGCTGTCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCCCTG 120
Db 61 AAGGCTGTCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCCCTG 120
QY 121 CTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGAGAACTGC 180
Db 121 CTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGAGAACTGC 180
QY 181 ACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGGCAGTTGGCCTGNTGACCGTC 240
Db 181 ACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGGCAGTTGGCCTGNTGACCGTC 240
QY 241 ATCAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 290

Db 241 ATCAGCAAAAGGCTGCAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 291
RESULT 4
US-10-252-157-273
Sequence 273, Application US/10252157
Publication No. US20030190640A1
GENERAL INFORMATION:
APPLICANT: Paris, Mary
APPLICANT: Pearson, Cecelia I.
TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: PA-0027-1 US
CURRENT APPLICATION NUMBER: US/10/252,157
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL Program
SEQ ID NO 273
LENGTH: 1028
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030190640A1 239797.3
US-10-252-157-273
Query Match 94.8%; Score 275; DB 15; Length 1028;
Best Local Similarity 98.3%; Pred. No. 1.3e-74;
Matches 286; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 CATTGAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCGACCCAGTGCACCATG 60
Db 1 CATTGAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCGACCCAGTGCACCATG 60
QY 61 AAGGCTGTCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCCCTG 120
Db 61 AAGGCTGTCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCCCTG 120
QY 121 CTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGAGAACTGC 180
Db 121 CTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGAGAACTGC 180
QY 181 ACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGGCAGTTGGCCTGNTGACCGTC 240
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QY 241 ATCAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 290
Db 241 ATCAGCAAAAGGCTGCAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 291

RESULT 5
US-09-080-140-2
Sequence 2, Application US/09080140
Publication No. US20040018553A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 31

APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherff, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 386
LENGTH: 990
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF043498
NAME/KEY: unsure
LOCATION: (1)..(981)
OTHER INFORMATION: n = a or c or g or t
US-10-240-425-386

Query Match 78.3%; Score 227; DB 13; Length 990;
Best Local Similarity 98.3%; Pred. No. 7.6e-60;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGCTGTGCTGCTTGCCTTTCATGCGAGGCTTGGCCCTGCAGCCAG 109
DB 10 CAGTGACCATGAAGCTGTGCTGCTTGCCTTTCATGCGAGGCTTGGCCCTGCAGCCAG 69
QY 110 GCACCTGCCCTGTGCTGCTACTCTCTCAAGCCAGCTGAGCAACGAGGACTGCCCTGCAGG 169
DB 70 GCACCTGCCCTGTGCTGCTACTCTCTCAAGCCAGCTGAGCAACGAGGACTGCCCTGCAGG 129
QY 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCGCATCCGCGCAGTTGGCC 229
DB 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCGCATCCGCGCAGTTGGCC 189
QY 230 TCNTGACCGCTCATCAGCAAA-GCTCAGCTTGAACCTGGTGGATGANTCAGAGGANTACT 288
DB 190 TCCTGACCGCTCATCAGCAAAAGCTGCAGCTTGAACCTGGTGGATGANTCAGAGGANTACT 249
QY 289 AC 290
DB 250 AC 251

RESULT 8
US-10-117-937-87
Sequence 87, Application US/10117937
Publication No. US2003020239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 602
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 87
LENGTH: 990
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(990)
OTHER INFORMATION: n = A,T,C or G
US-10-117-937-87

Query Match 78.3%; Score 227; DB 16; Length 990;
Best Local Similarity 98.3%; Pred. No. 7.6e-60;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGCTGTGCTGCTTGCCTTTCATGCGAGGCTTGGCCCTGCAGCCAG 109
DB 10 CAGTGACCATGAAGCTGTGCTGCTTGCCTTTCATGCGAGGCTTGGCCCTGCAGCCAG 69
QY 110 GCACCTGCCCTGTGCTGCTACTCTCTCAAGCCAGCTGAGCAACGAGGACTGCCCTGCAGG 169
DB 70 GCACCTGCCCTGTGCTGCTACTCTCTCAAGCCAGCTGAGCAACGAGGACTGCCCTGCAGG 129
QY 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCGCATCCGCGCAGTTGGCC 229
DB 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCGCATCCGCGCAGTTGGCC 189
QY 230 TCNTGACCGCTCATCAGCAAA-GCTCAGCTTGAACCTGGTGGATGANTCAGAGGANTACT 288
DB 190 TCCTGACCGCTCATCAGCAAAAGCTGCAGCTTGAACCTGGTGGATGANTCAGAGGANTACT 249
QY 289 AC 290
DB 250 AC 251

RESULT 9
US-10-188-832-168
Sequence 168, Application US/10188832
Publication No. US20040076955A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 168
LENGTH: 990
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (1)..(990)
OTHER INFORMATION: n = g, a, c or t
US-10-188-832-168

;; PRIOR APPLICATION NUMBER: 60/074,675
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: 60/113,230
;; PRIOR FILING DATE: 1998-12-21
;; PRIOR APPLICATION NUMBER: 60/120,536
;; PRIOR FILING DATE: 1999-02-17
;; PRIOR APPLICATION NUMBER: 60/124,658
;; PRIOR FILING DATE: 1999-03-16
;; PRIOR APPLICATION NUMBER: 09/038,261
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 09/203,939
;; PRIOR FILING DATE: 1998-12-02
;; PRIOR APPLICATION NUMBER: 09/251,835
;; PRIOR FILING DATE: 1999-02-17
;; PRIOR APPLICATION NUMBER: 09/308,503
;; PRIOR FILING DATE: 1999-05-25
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 998
;; TYPE: DNA
;; ORGANISM: HUMAN PSCA (hPSCA)
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (543)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (580)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (584)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (604)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (608)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (615)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (636)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (640)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (646)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (697)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (926)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-855-153-1
Query Match 78.3%; Score 227; DB 9; Length 998;
Best Local Similarity 98.3%; Pred. No. 7,6e-60;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGCGAGCTTGGCCCTGCAGCCAG 109
DB 10 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGCGAGCTTGGCCCTGCAGCCAG 69
QY 110 GCAGTCCCTGTGCTGCTACTCTGCAAGCCAGTGAGCAACGAGGACTGCCCTGCAGG 169
DB 70 GCAGTCCCTGTGCTGCTACTCTGCAAGCCAGTGAGCAACGAGGACTGCCCTGCAGG 129
QY 170 TGGAGAACTGCCACCCAGCTGGGGGAGCAGTGTGACCGCGGCGATCCGCGCAGTTGGCC 229
DB 130 TGGAGAACTGCCACCCAGCTGGGGGAGCAGTGTGACCGCGGCGATCCGCGCAGTTGGCC 189

QY 230 TCNTGACCGTCATCAGCAAA-GCTGCAGGTTCACTGCTGATGANTCAGGANTACT 288
DB 190 TCCTGACCGTCATCAGCAAAAGGCTGCAGCTTGAAGCTGCTGATGACTCAGGACTACT 249
QY 289 AC 290
DB 250 AC 251

RESULT 12
US-09-854-811-1
;; Sequence 1, Application US/09854811
;; Patent No. US20020119157A1
;; GENERAL INFORMATION:
;; APPLICANT: Reiter, Robert B.
;; APPLICANT: Witte, Owen N.
;; APPLICANT: Safran, Douglas C.
;; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
;; FILE REFERENCE: 30435 54US14
;; CURRENT APPLICATION NUMBER: US/09/854,811
;; CURRENT FILING DATE: 2001-05-14
;; PRIOR APPLICATION NUMBER: 09/564,329
;; PRIOR FILING DATE: 2000-05-03
;; PRIOR APPLICATION NUMBER: 09/359,326
;; PRIOR FILING DATE: 1999-07-20
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 998
;; TYPE: DNA
;; ORGANISM: HUMAN PSCA (hPSCA)
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (543)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (580)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (584)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (604)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (608)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (615)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (636)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (640)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (646)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (697)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
;; NAME/KEY: misc feature
;; LOCATION: (926)
;; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-854-811-1
Query Match 78.3%; Score 227; DB 9; Length 998;
Best Local Similarity 98.3%; Pred. No. 7,6e-60;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGCGAGCTTGGCCCTGCAGCCAG 109

Db 10 CAGTGACCATGAAGCTGTGCTGCTTGGCTTGTATGGCAGGCTTGGCCCTGCAGCCAG 69
QY 110 GCACTGCCCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACAGGAGCTGCTCTGCAGG 169
Db 70 GCACTGCCCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACAGGAGCTGCTCTGCAGG 129
QY 170 TGGAGAACTGCACCACTGCTGGGGAGAGCTGCTGACCGCGCGCATCCGGCAGCTTGGCC 229
Db 130 TGGAGAACTGCACCACTGCTGGGGAGAGCTGCTGACCGCGCGCATCCGGCAGCTTGGCC 189
QY 230 TCNTGACCGTTCATCAGCAAA-GCTGCACTTGAATCGTGGATGANTCAGAGANTACT 288
Db 190 TCCTGACCGTTCATCAGCAAAAGGCTGCACTTGAATCGTGGATGANTCAGAGANTACT 249
QY 289 AC 290
Db 250 AC 251

RESULT 13

US-09-934-773-1

; Sequence 1, Application US/09934773

; Patent No. US20020136689A1

; GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US14

; CURRENT APPLICATION NUMBER: US/09/934,773

; PRIORITY FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: 09/564,329

; PRIOR FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: 09/359,326

; PRIOR FILING DATE: 1998-07-20

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 60/113,230

; PRIOR FILING DATE: 1998-12-21

; PRIOR APPLICATION NUMBER: 60/120,536

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 60/124,658

; PRIOR FILING DATE: 1999-03-16

; PRIOR APPLICATION NUMBER: 09/038,261

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 09/203,939

; PRIOR FILING DATE: 1998-12-02

; PRIOR APPLICATION NUMBER: 09/251,835

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 09/308,503

; PRIOR FILING DATE: 1999-05-25

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; TYPE: DNA

; LENGTH: 998

; ORGANISM: HUMAN PSMA (hpsma)

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (543)

; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

; NAME/KEY: misc.feature

; LOCATION: (580)

; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

; NAME/KEY: misc.feature

; LOCATION: (584)

; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

; NAME/KEY: misc.feature

; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc.feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc.feature
; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc.feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc.feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc.feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc.feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc.feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; US-09-934-773-1

Query Match 78.3%; Score 227; DB 9; Length 998;

Best Local Similarity 98.3%; Pred. No. 7.6e-60;

Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 50 CAGTGACCATGAAGCTGTGCTTGGCTTGTATGGCAGGCTTGGCCCTGCAGCCAG 109
Db 10 CAGTGACCATGAAGCTGTGCTTGGCTTGTATGGCAGGCTTGGCCCTGCAGCCAG 69
QY 110 GCACTGCCCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACAGGAGCTGCTCTGCAGG 169
Db 70 GCACTGCCCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACAGGAGCTGCTCTGCAGG 129
QY 170 TGGAGAACTGCACCACTGCTGGGGAGAGCTGCTGACCGCGCGCATCCGGCAGCTTGGCC 229
Db 130 TGGAGAACTGCACCACTGCTGGGGAGAGCTGCTGACCGCGCGCATCCGGCAGCTTGGCC 189
QY 230 TCNTGACCGTTCATCAGCAAA-GCTGCACTTGAATCGTGGATGANTCAGAGANTACT 288
Db 190 TCCTGACCGTTCATCAGCAAAAGGCTGCACTTGAATCGTGGATGANTCAGAGANTACT 249
QY 289 AC 290
Db 250 AC 251

RESULT 14

US-09-963-620-1

; Sequence 1, Application US/09963620

; Patent No. US20020141941A1

; GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US14

; CURRENT APPLICATION NUMBER: US/09/963,620

; PRIORITY FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/564,329

; PRIOR FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: 09/359,326

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 60/113,230

PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 998
TYPE: DNA
ORGANISM: HUMAN PSCA (hPSCA)
FEATURE:
NAME/KEY: misc feature
LOCATION: {543}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {580}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {584}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {604}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {608}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {615}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {636}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {640}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {646}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {697}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {926}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-963-620-1
Query Match 78.3%; Score 227; DB 9; Length 998;
Best Local Similarity 98.3%; Pred No. 7,6e-60;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGGCTGCTGCTTGGCCCTTTGATGCGAGCTGGCCCTGCGAGCCAG 109
DB 10 CAGTGACCATGAAGGCTGCTGCTTGGCCCTTTGATGCGAGCTGGCCCTGCGAGCCAG 69
QY 110 GCACTGCCCTGCTGCTACTCTGCAAGCCAGCTGAGCAACGAGGACTGCCCTGCAGG 169
DB 70 GCACTGCCCTGCTGCTACTCTGCAAGCCAGCTGAGCAACGAGGACTGCCCTGCAGG 129
QY 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGAACCGCGGCATCCCGCAGTTGCC 229
DB 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGAACCGCGGCATCCCGCAGTTGCC 189
QY 230 TCTGACCGCTCATCAGCAA-CCTGCGCTTGAACCTGGATGATCAGGAGTACT 288

Db 190 TCTGACCGCTCATCAGCAAAGGCTGCGAGCTTGAACCTGGATGATCAGGAGTACT 249
QY 289 AC 290
Db 250 AC 251
RESULT 15
US-09-855-632-1
Sequence 1, Application US/09855632
Publication No: US20030113818A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Safran, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/855,632
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 998
TYPE: DNA
ORGANISM: HUMAN PSCA (hPSCA)
FEATURE:
NAME/KEY: misc feature
LOCATION: {543}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {580}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {584}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {604}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {608}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {615}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {636}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {640}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {646}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {697}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: {926}
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: {646}
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: {697}
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: {926}
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-855-632-1

Query Match 78.3%; Score 227; DB 10; Length 998;
Best Local Similarity 98.3%; Pred. No. 7.6e-60;
Matches 238; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 50 CAGTGACCATGAAGGCTGTGCTTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 109
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
10 CAGTGACCATGAAGGCTGTGCTTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 69
QY 110 GCATGCCCCCTGTGTACTCTGCAAGCCCAAGGTGAGCAACGAGACTGCTGCAGG 169
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
70 GCATGCCCCCTGTGTACTCTGCAAGCCCAAGGTGAGCAACGAGACTGCTGCAGG 129
QY 170 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCCGCGGCATCCGGCAGTTGGCC 229
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
130 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCCGCGGCATCCGGCAGTTGGCC 189
QY 230 TCNTGACCGTCATCAGCAAA-GCTGCAGCTTGAATGCGTGGATGANTCAGAGGANTACT 288
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
190 TCCTGACCGTCATCAGCAAAAGGCTGCAGCTTGAATGCGTGGATGACTCAGAGGANTACT 249
QY 289 AC 290
Db ||
250 AC 251

Search completed: September 18, 2004, 20:20:19
Job time : 219.341 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 05:54:35 ; Search time 1326.14 Seconds
(without alignments)
6530.246 Million cell updates/sec

Title: US-09-079-874-1
Perfect score: 290
Sequence: 1 CATTGAGCCATATAAGT.....ATGANTCAGCAGTACTAC 290
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_pig:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	273	94.1	424	12	BM768967 K-EST0052
2	273	94.1	470	13	BQ083505 K-EST0146
3	273	94.1	527	13	BQ083498 K-EST0146
4	272.4	93.9	843	14	CB997275 AGENCOURT

5	272.4	93.9	851	14	CB9993163
6	236	81.4	480	12	BM819937
7	236	81.4	550	14	CB147558
8	234.4	80.8	820	14	CB996183
9	233	80.3	827	12	BM018750
10	233	80.3	972	12	BM018834
11	232.4	80.1	547	12	BM828076
12	230.8	79.6	315	12	BM750435
13	225	77.6	682	12	BM042219
14	225	77.6	592	12	BM042219
15	225	77.6	1024	8	BC023582
16	223.4	77.0	990	11	BC048808
17	221.4	76.3	749	12	BM042052
18	219.4	75.7	924	13	BQ678675
19	219.4	75.7	857	13	BQ876328
20	219.4	75.7	970	13	BU179764
21	217.4	75.0	372	29	AY418122
22	217	74.8	901	13	BU173702
23	216	74.5	1009	13	BU168445
24	214	73.8	936	13	BU174241
25	209.8	72.3	571	12	BI763453
26	205	70.7	748	12	BG765417
27	167.4	57.7	850	13	BU157227
28	167.4	57.7	978	13	BQ680817
29	167	57.6	316	29	AY418123
30	146.8	50.6	885	12	BI761372
31	138	47.6	735	12	BM041997
32	134	46.2	922	13	BU168360
33	134	46.2	1096	13	BU838702
34	133	45.9	911	13	BU194301
35	133	45.9	924	13	BU174317
36	125.4	43.2	339	12	BI862705
37	111	38.3	985	13	BX416907
38	111	38.3	1200	13	BX404752
39	111	38.3	1201	13	BX402452
40	110.8	38.2	350	13	BY104399
41	110.8	38.2	373	13	BY084538
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44	110.8	38.2	386	13	BY088484
45	110.8	38.2	388	13	BY088363

ALIGNMENTS

RESULT 1
BM768967
LOCUS
DEFINITION K-EST0052116 S14K402 Homo sapiens CDNA clone S14K402-13-D04 5',
424 bp mRNA linear EST 04-MAR-2002
mRNA sequence.
ACCESSION BM768967
VERSION BM768967.1 GI:19098582
KEYWORDS EST,
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 424)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
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Korea Research Institute of Bioscience & Biotechnology
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 13 row: D column: 04
High quality sequence stop: 424.

High quality sequence stop: 424.

FEATURES

Location/Qualifiers
1. 424
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-13-D04"
/cell_line="K402"
/lab_host="Top10F"
/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 94.1%; Score 273; DB 12; Length 424;
Best Local Similarity 98.3%; Pred. No. 1.9e-50;
Matches 284; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 TTGTAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGATGACCATGAA 62
DB 3 TTGTAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGATGACCATGAA 62
QY 63 GGCTGTGCTGTGCTTGTGATGGCAGGCTTGGCCCTGACGAGGCACTGCGCTGCT 122
DB 63 GGCTGTGCTGTGCTTGTGATGGCAGGCTTGGCCCTGACGAGGCACTGCGCTGCT 122
QY 123 GTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGGAGAACTGCAC 182
DB 123 GTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGGAGAACTGCAC 182
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DB 183 CCAGCTGGGGAGCAGTGTGACCGCGCATCGCGCAGTTCGCTTCCTGACCGTCAAT 242
QY 243 CAGCAAAA-GCTGCAGCTTGAACCTGGTGATGANTCAGAGGANTACTAC 290
DB 243 CAGCAAAAGCTGCAGCTTGAACCTGGTGATGANTCAGAGGANTACTAC 291

RESULT 2

BQ083505
LOCUS K-EST0146186 S14K402 Homo sapiens cDNA clone S14K402-65-D08 5',
DEFINITION mRNA sequence.

ACCESSION BQ083505
VERSION BQ083505.1 GI:19942340
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 470)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE

JOURNAL

COMMENT

Contact: Kim YS
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Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 65 row: D column: 08

High quality sequence stop: 470.

FEATURES

Location/Qualifiers
1. 470

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S14K402-65-D08"

/cell_line="K402"

/lab_host="Top10F"

/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 94.1%; Score 273; DB 13; Length 470;
Best Local Similarity 98.3%; Pred. No. 2e-50;
Matches 284; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 TTGTAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGATGACCATGAA 62
DB 3 TTGTAGGCCATATAAGTCACCTGAGGCGCTCTCCACACAGCCGCCACGATGACCATGAA 62
QY 63 GGCTGTGCTGTGCTTGTGATGGCAGGCTTGGCCCTGACGAGGCACTGCGCTGCT 122
DB 63 GGCTGTGCTGTGCTTGTGATGGCAGGCTTGGCCCTGACGAGGCACTGCGCTGCT 122
QY 123 GTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGGAGAACTGCAC 182
DB 123 GTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCTCGAGGTGGAGAACTGCAC 182
QY 183 CCAGCTGGGGAGCAGTGTGACCGCGCATCGCGCAGTTCGCTTCCTGACCGTCAAT 242
DB 183 CCAGCTGGGGAGCAGTGTGACCGCGCATCGCGCAGTTCGCTTCCTGACCGTCAAT 242
QY 243 CAGCAAAA-GCTGCAGCTTGAACCTGGTGATGANTCAGAGGANTACTAC 290
DB 243 CAGCAAAAGCTGCAGCTTGAACCTGGTGATGANTCAGAGGANTACTAC 291

RESULT 3

BQ083498

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 65 row: C column: 11
High quality sequence stop: 527.
Location/Qualifiers
1. 527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-65-C11"
/cell_line="K402"
/lab_host="Top10P"
/clone_lib="S14K402"
/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDA360 row: p column: 20
High quality sequence stop: 612.
Location/Qualifiers
1. 843
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/db_xref="taxon:9606"
/clone="IMAGE:30336859"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamHI; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTATTTTATTTT-3', size-selected for average insert size 2.3 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

FEATURES
source
1. 843
Query Match 94.1%; Score 273; DB 13; Length 527;
Best Local Similarity 98.3%; Pred. No. 2.1e-50;
Matches 284; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 3 TTGTAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCACCCAGTGAACATGAA 62
DB 3 TTGTAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCACCCAGTGAACATGAA 62
QY 63 GGCTGTGCTGCTTGCCTCTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACCTGCCTGCT 122
DB 63 GGCTGTGCTGCTTGCCTCTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACCTGCCTGCT 122
QY 123 GTGCTACTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCGAGGTGGAGAACTGCAC 182
DB 123 GTGCTACTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCGAGGTGGAGAACTGCAC 182
QY 183 CCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTCTGACCGTCTAT 242
DB 183 CCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTCTGACCGTCTAT 242
QY 243 CAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 290
DB 243 CAGCAAAAGGCTGCAGCTTGAACCTGCGTGGATGACTCAGAGGACTACTAC 291

RESULT 4
CB997275
LOCUS
DEFINITION
AGENCOURT 13643348 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30336859 5', mRNA sequence.
CB997275
ACCESSION
CB997275.1 GI:30291795
EST.
KEYWORDS
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDA360 row: p column: 20
High quality sequence stop: 612.
Location/Qualifiers
1. 843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30336859"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamHI; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTATTTTATTTT-3', size-selected for average insert size 2.3 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

FEATURES
source
1. 843
Query Match 93.9%; Score 272.4; DB 14; Length 843;
Best Local Similarity 97.9%; Pred. No. 3.6e-50;
Matches 284; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 2 ATTTGAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCACCCAGTGAACATGA 61
DB 28 ATTTGAGGCCATATAAGTCACTGAGGNCCTCTCCACACAGCCACCCAGTGAACATGA 87
QY 62 AGGCTGTGCTGCTTGCCTCTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACCTGCCTGC 121
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QY 122 TGTCCTACTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCGAGGTGGAGAACTGCA 181
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QY 182 CCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTCTGACCGTCTCA 241
DB 208 CCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTCTGACCGTCTCA 267
QY 242 TCAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCAGAGGANTACTAC 290
DB 268 TCAGCAAAAGGCTGCAGCTTGAACCTGCGTGGATGACTCAGAGGACTACTAC 317

RESULT 5
CB993163
LOCUS
DEFINITION
AGENCOURT 13628816 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30338013 5', mRNA sequence.
CB993163
ACCESSION
CB993163.1 GI:30287683
EST.
KEYWORDS

CB147558
LOCUS K-EST0203584 L11SN354s1 550 bp mRNA linear EST 29-JAN-2003
DEFINITION K-EST0203584 L11SN354s1 Homo sapiens cDNA clone L11SN354s1-29-C07
5', mRNA sequence.

ACCESSION CB147558
VERSION CB147558.1 GI:28129015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsu@gmail.kr
Plate: 29 row: C column: 07
High quality sequence stop: 550.

FEATURES
source
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/db_xref="taxon:9606"
/clone="L11SN354s1-29-C07"
/sex="M"
/tissue_type="Liver"
/cell_type="Polygonal"
/cell_line="SNU-354"
/lab_host="Top10F"
/notes="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 - 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promoter as 5' primer and NidT14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtracted cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10F, with
electroporation method."

ORIGIN

Query Match 81.4%; Score 236; DB 14; Length 550;
Best Local Similarity 98.4%; Pred. No. 3.5e-42;
Matches 247; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

ORIGIN

Query Match 80.8%; Score 234.4; DB 14; Length 820;
Best Local Similarity 98.0%; Pred. No. 9.6e-42;
Matches 246; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 41 ACAGCCACAGTGAAGGCTGCTGCTTGCCTTGTGATGCAGGCTTGCC 100
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Db 1 ACAGCCACAGTGAAGGCTGCTGCTTGCCTTGTGATGCAGGCTTGCC 60
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QY 101 TGCAGCCAGGCACTGCCCTGCTGCTTCTCTGCAAGCCAGGTGAGCAACGAGGACT 160
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Db 61 TGCAGCCAGGCACTGCCCTGCTGCTTCTCTGCAAGCCAGGTGAGCAACGAGGACT 120
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|
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QY 161 GCTGTCAGTGGAGAACTGCAACCCAGCTGGGGAGCAGCTGTGGACCGGCATCCCGC 220
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Db 121 GCCTGAGGTGGAGAACTGCAACCCAGCTGGGGAGCAGCTGTGGACCGGCATCCCGC 180
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QY 221 CAGTTGGCTCTGTGACCGTCATCAGCAAA-GCTGCAGCTTGAACCTGCTGTGATGANTCAC 279
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|
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Db 181 CAGTTGGCTCTGTGACCGTCATCAGCAAAAGGCTGAGCTTGAACCTGCTGTGATGANTCAC 240
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QY 280 AGGANTACTAC 290
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|
Db 241 AGGACTACTAC 251
|
|
|

RESULT 8

CB996183
LOCUS AGENCOURT_13622529 NIH_MGC_148 Homo sapiens cDNA clone
DEFINITION IMAGE:30337181 5', mRNA sequence.

ACCESSION CB996183
VERSION CB996183.1 GI:30290703
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 820)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM361 row: n column: 06

High quality sequence stop: 597.

Location/Qualifiers

FEATURES

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/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-3ho1; Site 2: BamH1; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTT-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

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QY 41 ACAGCCACAGTACCATGAAGGCTGTGCTCTGCTCCCTGTGTGATGGCAGGCTTGGCCCTGC 100
Db 28 ACAGCCACAGTACCATGAAGGCTGTGCTCTGCTCCCTGTGTGATGGCAGGCTTGGCCCTGC 87
QY 101 TGAGCCAGGCACTGCGCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACT 160
Db 88 TGAGCCAGGCACTGCGCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACT 147
QY 161 GCTGAGGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTGGACCGCGGCATCCGCG 220
Db 148 GCTGAGGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTGGACCGCGGCATCCGCG 207
QY 221 CAGTTGGCTCTNTGACCGTCATCAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCAC 279
Db 208 CAGTTGGCTCTNTGACCGTCATCAGCAAAAGGCTGAGCTTGAACCTGCGTGGATGANTCAC 267
QY 280 AGGANTACTAC 290
Db 268 AGGACTACTAC 278

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RESULT 9
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LOCUS 603646652F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5428261 5',
DEFINITION mRNA sequence.
ACCESSION BM018750
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 827)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1895 row: g column: 14
High quality sequence stop: 810.
FEATURES
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_98"
/notes="Organ: Brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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Query Match 80.3%; Score 233; DB 12; Length 827;
Best Local Similarity 98.4%; Pred. No. 2e-41;
Matches 244; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 44 GCCACACGATGACCATGAAGGCTGTGCTCTGCTCCCTGTGTGATGGCAGGCTTGGCCCTGC 103
Db 2 GCCACACGATGACCATGAAGGCTGTGCTCTGCTCCCTGTGTGATGGCAGGCTTGGCCCTGC 61

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Db 2 GCCACACGATGACCATGAAGGCTGTGCTCTGCTCCCTGTGTGATGGCAGGCTTGGCCCTGC 61
QY 104 AGCCAGGCACTGCGCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCC 163
Db 62 AGCCAGGCACTGCGCTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCC 121
QY 164 TGAGGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTGGACCGCGGCATCCGCGCAG 223
Db 122 TGAGGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTGGACCGCGGCATCCGCGCAG 181
QY 224 TTGGCTCTNTGACCGTCATCAGCAAA-GCTGCAGCTTGAACCTGCGTGGATGANTCACAG 282
Db 182 TTGGCTCTNTGACCGTCATCAGCAAAAGGCTGAGCTTGAACCTGCGTGGATGANTCACAG 241
QY 283 ANTACTAC 290
Db 242 ACTACTAC 249

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RESULT 10
BM018834
LOCUS 603646752F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5428285 5',
DEFINITION mRNA sequence.
ACCESSION BM018834
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 972)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1895 row: h column: 14
High quality sequence stop: 831.
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:5428285"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_98"
/notes="Organ: Brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

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Query Match 80.3%; Score 233; DB 12; Length 972;
Best Local Similarity 98.4%; Pred. No. 2.1e-41;
Matches 244; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 44 GCCACACGATGACCATGAAGGCTGTGCTCTGCTCCCTGTGTGATGGCAGGCTTGGCCCTGC 103
Db 2 GCCACACGATGACCATGAAGGCTGTGCTCTGCTCCCTGTGTGATGGCAGGCTTGGCCCTGC 61

```


degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10P' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

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ORIGIN
Query Match          79.6%; Score 230.8; DB 12; Length 315;
Best Local Similarity 97.6%; Pred. No. 3.9e-41;
Matches 243; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 43 AGCCACCAAGTACCATGAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGCCCTG 102
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QY 103 CAGCCAGGCACTGCCCTGCTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 162
    |||
Db 61 CAGCCAGGCACTGCCCTGCTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 120

QY 163 CTGCGAGTGGAGAACTGACCCAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCA 222
    |||
Db 121 CTGCGAGTGGAGAACTGACCCAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCA 180

QY 223 GTTGCCCTCAGTACATCAGCAAA-GCTGCAGCTTGAACCTGGTGGATGANTCAG 281
    |||
Db 181 GTTGCCCTCAGTACATCAGCAAAAGCTGACGCTTGAACCTGGTGGATGANTCAG 240

QY 282 GANTACTAC 290
Db 241 GACTACTAC 249

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RESULT 13
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LOCUS
DEFINITION
603616172F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5557096 5',
mRNA sequence.
ACCESSION
BM042219
VERSION
BM042219.1 GI:16771486
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 682)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM2021 row: o column: 17
High quality sequence stop: 678.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5557096"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:

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FEATURES
source

```

GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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ORIGIN
Query Match          77.6%; Score 225; DB 12; Length 682;
Best Local Similarity 98.3%; Pred. No. 1.1e-39;
Matches 236; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 52 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGCCCTGAGCCAGGC 111
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Db 2 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGCCCTGAGCCAGGC 61

QY 112 ACTGCCCTGCTGTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCTGAGGTG 171
    |||
Db 62 ACTGCCCTGCTGTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCTGAGGTG 121

QY 172 GAGAACTGCAACGAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCATTTGGCCTC 231
    |||
Db 122 GAGAACTGCAACGAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCATTTGGCCTC 181

QY 232 NTGACCGTCTATCAGCAAA-GCTGCAGCTTGAACCTGGTGGATGANTCAGGANTACTAC 290
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Db 182 CTGACCGTCTATCAGCAAAAGGCTGACGCTTGAACCTGGTGGATGANTCAGGANTACTAC 241

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RESULT 14
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LOCUS
DEFINITION
602717425F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4840974 5',
mRNA sequence.
ACCESSION
BG761095
VERSION
BG761095.1 GI:14071748
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 692)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM1673 row: a column: 07
High quality sequence stop: 690.
Location/Qualifiers
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/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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FEATURES
source

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Search completed: September 18, 2004, 19:14:20
Job time : 1331.14 secs

Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:35:58 ; Search time 1467.19 Seconds
(without alignments)
8655.682 Million cell updates/sec

Title: US-09-079-874-2

Perfect score: 293
Sequence: 1 GAGGCCCTTCACACAGC.....AGAGAACATCACGTGCTGT 293

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sy.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rdt.*
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40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	289.8	98.9	373	6	AX884747	AX884747 Sequence
2	289.8	98.9	373	6	BD024357	BD024357 Sequence
3	289.8	98.9	373	6	BD076969	BD076969 5' EST of
4	278	94.9	946	9	HS2297436	AJ297436 Homo sapi
5	274.4	93.7	979	6	BD076397	BD076397 Human pro
6	269	91.8	990	6	AX014204	AX014204 Sequence
7	269	91.8	990	6	BD205072	BD205072 Human nuc
8	269	91.8	990	9	AF043498	AF043498 Homo sapi
9	269	91.8	998	6	AR162849	AR162849 Sequence
10	269	91.8	998	6	AR302232	AR302232 Sequence
11	269	91.8	998	6	AX080304	AX080304 Sequence
12	269	91.8	998	6	BD193367	BD193367 Prostate
13	267	91.1	288	6	AR026990	AR026990 Sequence
14	267	91.1	494	6	AR026974	AR026974 Sequence
15	267	91.1	1015	9	BC023582	BC023582 Homo sapi
16	265.8	90.7	998	6	BD264314	BD264314 PSCA: pro
17	261	89.1	372	6	AX155553	AX155553 Sequence
18	259.4	88.5	369	6	BD076387	BD076387 Human pro
19	250	85.3	960	6	AR410610	AR410610 Sequence
20	250	85.3	960	6	AX201328	AX201328 Sequence
21	250	85.3	960	6	AX697426	AX697426 Sequence
22	250	85.3	960	6	BD075381	BD075381 Secretory
23	250	85.3	960	6	BD172241	BD172241 Secreted
24	250	85.3	960	6	BD172560	BD172560 Secreted
25	250	85.3	960	6	BD172879	BD172879 Secreted
26	250	85.3	960	6	BD173198	BD173198 Secreted
27	250	85.3	960	6	BD175232	BD175232 Secretory
28	250	85.3	960	9	AY358912	AY358912 Homo sapi
29	241.8	82.5	372	6	AX155567	AX155567 Sequence
30	240.2	82.0	372	6	AX155569	AX155569 Sequence
31	218.4	74.5	232	6	AR026992	AR026992 Sequence
32	218	74.4	286	6	AR026988	AR026988 Sequence
33	148.8	50.8	864	10	AF319173	AF319173 Mus muscu
34	144.8	49.4	441	6	AR162850	AR162850 Sequence
35	144.8	49.4	441	6	BD264315	BD264315 PSCA: pro
36	144.8	49.4	441	6	AR302233	AR302233 Sequence
37	144.8	49.4	441	6	AX080306	AX080306 Sequence
38	144.8	49.4	441	6	BD193368	BD193368 Prostate
39	112.4	38.4	2532	6	AX747544	AX747544 Sequence
40	112.4	38.4	2532	9	AK092432	AK092432 Homo sapi
41	112.4	38.4	100079	9	AC108002	AC108002 Homo sapi
42	112.4	38.4	103247	2	AF176678	AF176678 Homo sapi
43	112.4	38.4	105156	2	AF235094	AF235094 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AX884747 373 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 610 from Patent EP1033401.
ACCESSION AX884747
VERSION AX884747.1 GI:40040217
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 610 06-SEP-2000;

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    109..5372
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    /codon_start=1
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    /db_xref="GI:40040218"
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ORIGIN
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Best Local Similarity 98.3%; Pred. No. 1.4e-49;
Matches 288; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGCCCTCTCCACACAGCCACCAGTGCACATGACGCTGCTGCTTGCCTGTGA 60
DB 77 GAGGCCCTCTCCACACAGCCACCAGTGCACATGACGCTGCTGCTTGCCTGTGA 136
QY 61 TGCGAGGCTTGCCCTCGCAGCCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 137 GAGGCCCTCTCCACACAGCCACCAGTGCACATGACGCTGCTGCTGCTGCTGCTG 196
QY 121 TGAGCAACGAGAGTCCCTGCGAGCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCT 180
DB 197 TGRGCAACGAGAGTCCCTGCGAGCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCT 256
QY 181 TGAGCAACGAGAGTCCCTGCGAGCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCT 240
DB 257 TGRGCAACGAGAGTCCCTGCGAGCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCT 316
QY 241 GCGTGGATGACTCAGAGGACTACTACGTGGGCAAGAAACATCATCGTGTCTGT 293
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RESULT 2
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LOCUS             373 bp DNA linear PAT 27-AUG-2002
DEFINITION       Sequence tag and encoded human protein.
ACCESSION        BD024357
VERSION          BD024357.1 GI:22565580
KEYWORDS         JP 2001269182-A/603.
SOURCE            Homo sapiens (human)
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  AUTHORS        Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE          Sequence tag and encoded human protein.
  JOURNAL        Patent: JP 2001269182-A 603 02-OCT-2001;
                  GENSET
COMMENT
  OS            Homo sapiens (human)
  PN            JP 2001269182-A/603
  PD            02-OCT-2001
  PR            24-FEB-2000 JP 2000118773
  PI            JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
  PC            JORDAN
  PC            C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
  PC            C12N5/10,
  PC            C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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  FH            Key Location/Qualifiers
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FEATURES             Location/Qualifiers
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Query Match      98.9%; Score 289.8; DB 6; Length 373;
Best Local Similarity 98.3%; Pred. No. 1.4e-49;
Matches 288; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGCCCTCTCCACACAGCCACCAGTGCACATGACGCTGCTGCTGCTGCTGCTGCTGA 60
DB 77 GAGGCCCTCTCCACACAGCCACCAGTGCACATGACGCTGCTGCTGCTGCTGCTGCTGA 136
QY 61 TGCGAGGCTTGCCCTCGCAGCCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 137 TGCAGGCTTGCCCTCGCAGCCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 196
QY 121 TGAGCAACGAGAGTCCCTGCGAGCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 197 TGRGCAACGAGAGTCCCTGCGAGCAGCACTGCCTGCTGCTGCTGCTGCTGCTGCTG 256
QY 181 CCGCGGCATCCGCGAGTGGCCCTCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 257 CCGCGGCATCCGCGAGTGGCCCTCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
QY 241 GCGTGGATGACTCAGAGGACTACTACGTGGGCAAGAAACATCATCGTGTCTGT 293
DB 317 GCGTGGATGACTCAGAGGACTACTACGTGGGCAAGAAACATCATCGTGTCTGT 369

RESULT 3
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LOCUS             373 bp DNA linear PAT 27-AUG-2002
DEFINITION       5' EST of secretory protein expressed in prostate.
ACCESSION        BD076969
VERSION          BD076969.1 GI:22622572
KEYWORDS         JP 2001512013-A/216.
SOURCE            Homo sapiens (human)
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  AUTHORS        Edwards,J.B.D.M., Duclair,A. and Lacroix,B.
  TITLE          5' EST of secretory protein expressed in prostate
  JOURNAL        Patent: JP 2001512013-A 216 21-AUG-2001;
                  GENSET
COMMENT
  OS            Homo sapiens (human)
  PN            JP 2001512013-A/216
  PD            21-AUG-2001
  PR            31-JUL-1998 JP 2000505291
  PR            01-AUG-1997 US 08/905144
  PI            JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLAIR, BRUNO PI
  PC            LACROIX
  PC            C12N15/09, C07K14/47, C12P21/02, C12Q1/02, C12Q1/68, C12N15/00 CC
  CC            blastn
  CC            identity 98
  CC            region 404..466
  CC            id AA158879
  CC            est
  CC            Von Heijne matrix
  CC            score 7.5
  CC            seq AVLLALLMAGLAL/QP
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  FT            misc feature 308..370
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  FT            Location/Qualifiers
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Query Match 98.9%; Score 289.8; DB 6; Length 373;
Best Local Similarity 98.3%; Pred. No. 1.4e-49;
Matches 288; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGCCCTCTCCACACAGCCACAGCCAGTCAGCATGAGGCTGTGCTTGCCTTGGCCCTGTGA 60
DB 78 GAGGCCCTCTCCACACAGCCACAGCCAGTCAGCATGAGGCTGTGCTTGCCTTGGCCCTGTGA 137
QY 61 TGGCAGGCTTGGCCCTCGAGCCAGGCACTGCGCTGCTGTGCTTCTCTGCAAAAGCCAGG 120
DB 138 TGGCAGGCTTGGCCCTCGAGCCAGGCACTGCGCTGCTGTGCTTCTCTGGAAGCCAGG 197
QY 121 TGAGCAAGAGGACTGCTGCTGAGGTGGAGAACTGACCCAGCTGGGGAGGAGTGGTGA 180
DB 198 TGGCAAGAGGACTGCTGCTGAGGTGGAGAACTGACCCAGCTGGGGAGGAGTGGTGA 257
QY 181 CGCGCGCATCGCGCAGTGTGGCTTCCCTGACCGTTCATCAGCAAAAGGCTGCACTTGA 240
DB 258 CGCGCGCATCGCGCAGTGTGGCTTCCCTGACCGTTCATCAGCAAAAGGCTGCACTTGA 317
QY 241 GCGTGAGTACTCAGAGCACTACTAGTGGGCAAGAGAAATACAGTGTCTGT 293
DB 318 GCGTGATSACTCAGAGCACTACTAGTGGGCAAGAGAAATACAGTGTCTGT 370

RESULT 4
HSA297436 946 bp mRNA linear PRI 13-OCT-2000
LOCUS
DEFINITION Homo sapiens mRNA for prostate stem cell antigen (PSCA gene).
ACCESSION AJ297436
VERSION AJ297436.1 GI:9367211
KEYWORDS prostate stem cell antigen; PSCA gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Bahrenberg G., Brauers A., Joest H.G. and Jakse, G.
Reduced expression of PSCA, a member of the LY-6 family of cell
surface antigens, in bladder, esophagus, and stomach tumors
Biochem. Biophys. Res. Commun. 275 (3), 783-788 (2000)
20431743
PUBMED 10973799
REFERENCE 2 (bases 1 to 946)
Bahrenberg G.
Direct Submission
Submitted (12-JUL-2000) Bahrenberg G., Institut fuer Pharmakologie
und Toxikologie, RWTH Aachen, Wendlingweg2, Aachen, NRW, 52057,
GERMANY
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20. .391
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gene
CDS

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Location/Qualifiers
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Best Local Similarity 93.6%; Pred. No. 1.8e-46;
Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 AGCCACAGTGACCATCAGGCTGTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTG 77

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ORIGIN

Query Match 94.9%; Score 278; DB 9; Length 946;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ACAGCCACAGTGCATGAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCC 75
DB 3 ACAGCCACAGTGCATGAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCC 82
QY 76 TGACAGCAGGCACTGCGCTGCTGTGCTTCTCTGCAAAAGCCAGGTGAGCAAGGACT 135
DB 63 TGACAGCAGGCACTGCGCTGCTGTGCTTCTCTGCAAAAGCCAGGTGAGCAAGGACT 122
QY 136 GCGTGAGTGGAGAACTGACCCAGCTGGGGAGGAGTGTGACCGCGGCATCCGG 195
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QY 196 CAGTTGGCTCTCTGACCGTTCATCAGCAAAAGGCTGCACTTGAACCTCGTGGATCACTAC 255
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QY 256 AGGACTACTACGTGGGCAAGAGAAATACATCAGTGTCTGT 293
DB 243 AGGACTACTACGTGGGCAAGAGAAATACATCAGTGTCTGT 280

RESULT 5
BD076397 979 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Human protein having transmembrane domain and DNA encoding the
same.
ACCESSION BD076397
VERSION BD076397.1 GI:22622000
KEYWORDS JP 2001519154-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Kato S., Kimura T., Sekine S. and Kobayashi M.
Human protein having transmembrane domain and DNA encoding the same
Patent: JP 2001519154-A 11 23-OCT-2001;
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
COMMENT OS Homo sapiens (human)
PN JP 2001519154-A/11
PD 23-OCT-2001
PF 05-OCT-1998 JP 2000515001
PI SEISHI KATO, TOMOKO KIMURA, SHINGO SEKINE, MIDORI KOBAYASHI PC
C12N15/09, C07K14/47, C12N15/10, C12N15/00, C12N5/00 CC Human protein
having transmembrane domain
and DNA encoding the
same
CC same
FH Key Location/Qualifiers
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/organism="Homo sapiens"
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1. .979
Location/Qualifiers
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ORIGIN

Query Match 93.7%; Score 274.4; DB 6; Length 979;
Best Local Similarity 93.6%; Pred. No. 1.8e-46;
Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 AGCCACAGTGACCATCAGGCTGTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTG 77

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Db      1 AGCCACCAAGTACCATGAAGGCTGTGCTTGCCTTTCATGCGAGGCTTGCCCTG 60
QY      78 CAGCAGGACACGCTGCTGTGCTTACTCTCTGCAAGCCAGGTCAGCAAGAGGACTGC 137
Db      61 CAGCCAGGACGCTGCTGTGCTTACTCTCTGCAAGCCAGGTCAGCAAGAGGACTGC 120
QY      138 CTCGAGGTGAGAACTGCACCCAGTGGGGAGGAGTCTGAGCCGCGCATCCGGCA 197
Db      121 CTCGAGGTGAGAACTGCACCCAGTGGGGAGGAGTCTGAGCCGCGCATCCGGCA 180
QY      198 GTTGGCTCTCAGCGTCTATCAGCAAGCTGCAGCTTGAAGTGGTGAATCACTCAG 257
Db      181 GTTGGCTCTCAGCGTCTATCAGCAAGCTGCAGCTTGAAGTGGTGAATCACTCAG 240
QY      258 GACTACTAGTGGGCAAGAAACATCAGTGTCTGT 293
Db      241 GACTACTAGTGGGCAAGAAACATCAGTGTCTGT 276

RESULT 6
LOCUS   AX014204
DEFINITION Sequence 108 from Patent WO954447.
ACCESSION AX014204
VERSION  AX014204.1 GI:10040611
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
        Pilarsky,C.
TITLE    Human nucleic acid sequences of bladder tumour tissue
JOURNAL  Patent: WO 954447-A 108 28-OCT-1999;
        SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
        BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
        (DE); PILARSKY CHRISTIAN (DE)
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e-45;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      25 CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGCGAGGCTTGCCCTCGAGCCAG 84
Db      10 CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGCGAGGCTTGCCCTCGAGCCAG 69
QY      85 GCATGCGCTGTGCTACTCTCTGCAAGCCAGGTCAGCAAGAGGACTGCTTGAGG 144
Db      70 GCATGCGCTGTGCTACTCTCTGCAAGCCAGGTCAGCAAGAGGACTGCTTGAGG 129
QY      145 TGGAGAACTGCACCCAGTGGGGAGGAGTGTGACCGCGGCATCCGCGCAGTTGGCC 204
Db      130 TGGAGAACTGCACCCAGTGGGGAGGAGTGTGACCGCGGCATCCGCGCAGTTGGCC 189
QY      205 TCCTGACCGTCTATCAGCAAGGCTGCAGTTGAATGCTGGTGAATCACTCAGGACT 264
Db      190 TCCTGACCGTCTATCAGCAAGGCTGCAGTTGAATGCTGGTGAATCACTCAGGACT 249
QY      265 ACGTGGGCAAGAGAACATCAGTGTCTGT 293
Db      250 ACGTGGGCAAGAGAACATCAGTGTCTGT 278

RESULT 7
LOCUS   BD205072
DEFINITION Human nucleic acid sequence originating in cystic cancer tissue.
ACCESSION BD205072
VERSION  BD205072.1 GI:33014842
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and
        Rosenthal,A.
TITLE    Human nucleic acid sequence originating in cystic cancer tissue
JOURNAL  Patent: JP 2002512023-A 26 23-APR-2002;
        METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
        OS Homo sapiens (human)
        PN JP 2002512023-A/26
        PD 23-APR-2002
        PR 15-APR-1999 JP 2000544779
        PR 21-APR-1998 DE 198 18 619 3
        PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
        PI EDGAR DAHL,
        PI ANDRE ROSENTHAL
        PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P13/10,
        PC A61P35/00,
        PC C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12P21/08, C12Q1/68, PC
        C12N15/00,
        PC A61K37/02, C12N5/00
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        FH tissue
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FEATURES             Location/Qualifiers
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Query Match      91.8%; Score 269; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 2.3e-45;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      25 CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGCGAGGCTTGCCCTCGAGCCAG 84
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QY      85 GCATGCGCTGTGCTACTCTCTGCAAGCCAGGTCAGCAAGAGGACTGCTTGAGG 144
Db      70 GCATGCGCTGTGCTACTCTCTGCAAGCCAGGTCAGCAAGAGGACTGCTTGAGG 129
QY      145 TGGAGAACTGCACCCAGTGGGGAGGAGTGTGACCGCGGCATCCGCGCAGTTGGCC 204
Db      130 TGGAGAACTGCACCCAGTGGGGAGGAGTGTGACCGCGGCATCCGCGCAGTTGGCC 189
QY      205 TCCTGACCGTCTATCAGCAAGGCTGCAGTTGAATGCTGGTGAATCACTCAGGACT 264
Db      190 TCCTGACCGTCTATCAGCAAGGCTGCAGTTGAATGCTGGTGAATCACTCAGGACT 249
QY      265 ACGTGGGCAAGAGAACATCAGTGTCTGT 293
Db      250 ACGTGGGCAAGAGAACATCAGTGTCTGT 278

RESULT 8
LOCUS   AF043498
DEFINITION Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds.
ACCESSION AF043498
VERSION  AF043498.1 GI:2909843
KEYWORDS
SOURCE  Homo sapiens (human)

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ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 990)
AUTHORS	Reiter,R.E., Gu,Z., Watabe,T., Thomas,G., Kinga,S., Davis,E., Wahl,M., Nisitani,S., Yamashiro,J., Le Beau,M.M., Losa,M. and Witte,O.N.
TITLE	Prostate stem cell antigen: a cell surface marker overexpressed in prostate cancer
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (4), 1735-1740 (1998)
MEDLINE	98132661
PUBMED	9465086
REFERENCE	2 (bases 1 to 990)
AUTHORS	Reiter,R.E.
TITLE	Direct Submission
JOURNAL	Submitted (19-JAN-1998) Urology, UCLA, 66-134 CHS 10833 Le Conte Ave., Los Angeles, CA 90095, USA
FEATURES	<p>Location/Qualifiers</p> <p>1..990</p> <p>gene</p> <p>1..990</p> <p>CDs</p> <p>18..389</p> <p> <code>/organism="Homo sapiens"</code> <code>/mol_type="mRNA"</code> <code>/db_xref="taxon:9606"</code> <code>/chromosome="8"</code> <code>/map="8q24.2"</code> <code>/notes="LAPC-4 prostate cancer xenograft"</code> <code>/gene="PSCA"</code> <code>/gene="PSCA"</code> <code>/gene="PSCA"</code> <code>/note="GPI-anchored cell surface protein"</code> <code>/codon_start=1</code> <code>/product="prostate stem cell antigen"</code> <code>/protein_id="AAC39607.1"</code> <code>/db_xref="GI:2909844"</code> <code>/translation="MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCIQVENCITQLGECWTARIRAVGLLTIVISGCSLNCVDDSDQYIVGKKNTCCDTLCLNAGAHALQPLAAAILALLPALGLLLWGPQL"</code> </p>
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Best Local Similarity	100.0%; Pred. No. 2.3e-45;
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Qy	25 CAGTGACCATGAAGCGTGTGCTGTTCCTCTTTGATGGCAGGCTTGGCCCTGCAGCCAG 84
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Qy	85 GCATGCGCCTGCTGTGCTACTCTTCGAAAGCCAGGTGAGCAACGAGGACTGCTCTGCAGG 144
Db	70 GCATGCGCCTGCTGTGCTACTCTTCGAAAGCCAGGTGAGCAACGAGGACTGCTCTGCAGG 129
Qy	145 TGGAGAACTGACCCAGCTGGGGGAGCAGTCTGGACCGCGCGCATCGGCAGCTTGCC 204
Db	130 TGGAGAACTGACCCAGCTGGGGGAGCAGTCTGGACCGCGCGCATCGGCAGCTTGCC 189
Qy	205 TCCTGACCGTCAATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGCAGGACTACT 264
Db	190 TCCTGACCGTCAATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGCAGGACTACT 249
Qy	265 ACCTGGGGCAGAAGAACATCACGTGCTGT 293
Db	250 ACCTGGGGCAGAAGAACATCACGTGCTGT 278
RESULT 9	
AR162849	
LOCUS	AR162849 998 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 1 from patent US 6258939.
ACCESSION	AR162849
VERSION	AR162849.1 GI:16230194
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.

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QY      265 ACGTGGGCAAGAGAACATCAGTGCTGT 293
Db      250 ACGTGGGCAAGAGAACATCAGTGCTGT 278

RESULT 11
AX080304
LOCUS   AX080304
DEFINITION Sequence 1 from Patent WO0105427.
ACCESSION AX080304
VERSION  AX080304.1 GI:13159773
SOURCE  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
  1
  Reiter,R., Witte,O., Saffran,D.C. and Jakobovits,A.
  PscA: prostate stem cell antigen and uses thereof
  Patent: WO 0105427-A 1 25-JAN-2001;
  JOURNAL THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) ; Urogenesys, Inc.
  (US)

FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.3e-45;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGCCCTGCAGCCAG 84
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QY      85 GCATGCCCTGTGCTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 144
Db      70 GCATGCCCTGTGCTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 129
QY      145 TGGAGACTGCACCCAGCTGGGGAGCAGTGTGACCGCGGCATCCGCGACTTGSCC 204
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QY      205 TCCTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 264
Db      190 TCCTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 249
QY      265 ACGTGGGCAAGAGAACATCAGTGCTGT 293
Db      250 ACGTGGGCAAGAGAACATCAGTGCTGT 278

RESULT 12
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LOCUS   BD193367
DEFINITION Prostate stem cell antigen.
ACCESSION BD193367
VERSION  BD193367.1 GI:33003106
KEYWORDS JP 2002511740-A/1.
SOURCE  unidentified
ORGANISM
  unidentified.
  1 (bases 1 to 998)
  Reiter,R. and Witte,O.
  Prostate stem cell antigen
  Patent: JP 2002511740-A 1 16-APR-2002;
  JOURNAL THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
  OS Unidentified

Db      190 TCCTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 249
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RESULT 13
AR026990
LOCUS   AR026990
DEFINITION Sequence 23 from patent US 5856136.
ACCESSION AR026990
VERSION  AR026990.1 GI:5937830
KEYWORDS
SOURCE  Unknown.
ORGANISM
  Unknown.
  Unclassified.
  1 (bases 1 to 288)
  Au-Young,J.
  Human stem cell antigens
  Patent: US 5856136-A 23 05-JAN-1999;
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ORIGIN
Query Match          91.1%; Score 267; DB 6; Length 288;
Best Local Similarity 100.0%; Pred. No. 7e-45;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGCCCTGCAGCCAGC 86
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PN      JP 2002511740-A/1
PD      16-APR-2002
PF      10-MAR-1998 JP 1998539713
PR      10-MAR-1997 US 08/814279,12-JAN-1998 US 60/071141 PR
13-FEB-1998 US 60/074675
P1      ROBERT REITER,OWEN WITTE
PC      C07K7/08,C07K16/28,C12Q1/68,G01N33/53
CC      Strandedness: Single;
CC      Topology: Linear;
CC      Human PSCA nucleotide sequence
FH      Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e-45;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      85 GCATGCCCTGTGCTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 144
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QY      205 TCCTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 264
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Db      250 ACGTGGGCAAGAGAACATCAGTGCTGT 278

RESULT 13
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LOCUS   AR026990
DEFINITION Sequence 23 from patent US 5856136.
ACCESSION AR026990
VERSION  AR026990.1 GI:5937830
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SOURCE  Unknown.
ORGANISM
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  Au-Young,J.
  Human stem cell antigens
  Patent: US 5856136-A 23 05-JAN-1999;
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Best Local Similarity 100.0%; Pred. No. 7e-45;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGCCCTGCAGCCAGC 86
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ORIGIN

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Query Match      91.1%; Score 267; DB 9; Length 1015;
Best Local Similarity 100.0%; Pred.No. 5.9e-45;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 86
Db 1 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
QY 87 ACTGCCCTGCTGTCTACTCTCGAAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 146
Db 61 ACTGCCCTGCTGTCTACTCTCGAAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 120
QY 147 GAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCATCCGCGCAGTTGGGCTC 206
Db 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCATCCGCGCAGTTGGGCTC 180
QY 207 CTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGGATGACTCACAGGACTACTAC 266
Db 181 CTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGGATGACTCACAGGACTACTAC 240
QY 267 GTGGGCAAGAGACATCACGTGCTGT 293
Db 241 GTGGGCAAGAGACATCACGTGCTGT 267

```

Search completed: September 18, 2004, 13:27:05
Job time : 1467.19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:33:41 ; Search time 191.537 Seconds
(without alignments)
6498.587 Million cell updates/sec

Title: US-09-079-874-2

Perfect score: 293
Sequence: 1 GAGGCCCTCTCCACACAGC.....AGAGAACATCACGTGCTGT 293

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002s: *
7: Geneseqn2003as: *
8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	293	100.0	293	2	AAV80387 Nucleotid
2	293	100.0	293	2	AAV68604 Human P51
3	293	100.0	1023	2	AAV80397 Consensus
4	293	100.0	1023	2	AAV68613 Human P51
5	293	100.0	1023	2	AAV68614 Human P51
6	293	100.0	1028	9	AD853926 Human pro
7	289.8	98.9	373	2	AAx40622 Human sec
8	289.8	98.9	373	3	AAc00612 Human sec
9	274.4	93.7	979	2	AAx36801 Human tra
10	269	91.8	279	2	AAV80388 Nucleotid
11	269	91.8	279	2	AAV80388 Nucleotid
12	269	91.8	990	7	AAv68605 Human P51
13	269	91.8	990	7	AAc51040 Human bla
14	269	91.8	990	7	ABq83853 Human PSC
15	269	91.8	990	9	Adc09589 PSCA cDNA
16	269	91.8	998	4	ABK09980 Human pro
17	267.4	91.3	998	5	AAf77971 Human pro
18	267.4	91.3	998	3	AAV33691 Human pro
19	267	91.1	288	3	AAa48374 Human pro
20	267	91.1	288	2	AAV38061 Human ste
21	267	91.1	494	2	AAV38045 Human ste
22	267	91.1	972	2	AAV80396 Nucleotid
23	261	89.1	372	4	AAa08171 Human tra
24	259.4	88.5	369	2	AAx36800 Human tra

ALIGNMENTS

RESULT 1

AAV80387
ID AAV80387 standard; DNA; 293 BP.

XX AAV80387;

DT 23-FEB-1999 (first entry)

DE Nucleotide sequence of UT116 gene-specific clone 2804743.

KW UT116; urinary tract; epitope; antigen; detection; diagnosing;
KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
KW metastasis; ss.

OS Homo sapiens.

PN WO9851824-A1.

XX 19-NOV-1998.

PD 15-MAY-1998; 98WO-US009972.

PR 15-MAY-1997; 97US-00856652.

XX (ABBO) ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
PI Stroupe SD;

XX WPI; 1999-045237/04.

XX New method for detecting diseases of the urinary tract - comprises use of
PT a UT116 polynucleotide, protein or antibodies, used for preventing and
treating urinary tract infections and cancer.

Claim 1; Fig 1A-C; 113pp; English.

XX Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
sequences of the UT116 gene-specific clones derived from urinary tract
tissue. The invention relates to a method of detecting the presence of a
target UT116 polynucleotide in a test sample using these UT116-specific
sequences. Host cells transfected with an expression vector containing
the UT116 gene can be used to produce a UT116 polypeptide recombinantly.
This polypeptide has at least one UT116 epitope which can be used in a
method for detecting UT116 antigen in a test sample. The polynucleotides

24 250 85.3 290 2 AAV80386
25 250 85.3 290 2 AAV68603
26 250 85.3 960 3 AAX52217
27 250 85.3 960 3 ADC78337
28 250 85.3 960 4 AAF72375
29 250 85.3 960 6 ABK40257
30 250 85.3 960 7 ACA58909
31 250 85.3 960 7 ACA58306
32 250 85.3 960 7 ACA60013
33 250 85.3 960 7 ACD07413
34 250 85.3 960 7 ABX71461
35 250 85.3 960 7 ACH06793
36 250 85.3 960 7 ABX96030
37 250 85.3 960 7 ACA05351
38 250 85.3 960 7 ACD20018
39 250 85.3 960 7 ACA54821
40 250 85.3 960 8 ACD19656
41 250 85.3 960 8 ADB29222
42 250 85.3 960 8 ADA18078
43 250 85.3 960 8 ACD66803
44 250 85.3 960 8 ACD82964
45 250 85.3 960 8 ADA16053

AAV80386 Nucleotid
AAV68603 Human P51
AAX52217 Protein P
ADC78337 Human PRO
AAF72375 Human PRO
ABK40257 cDNA enco
ACA58909 Human PRO
ACA58306 cDNA enco
ACA60013 Human cDN
ACD07413 Novel hum
ABX71461 Human cDN
ACH06793 Human sec
ABX96030 Human sec
ACA05351 cDNA enco
ACD20018 Human hum
ACA54821 Novel hum
ACD19656 Human sec
ADB29222 Human sec
ADA18078 Human sec
ACD66803 Human cDN
ACD82964 Human PRO
ADA16053 Human sec


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PA (ABBO ) ABBOTT LAB.
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
PI Stroupe SD;
XX WPI; 1999-045237/04.
DR P-PSDB; AAV86024.
XX
XX New method for detecting diseases of the urinary tract - comprises use of
PT a Utl16 polynucleotide, protein or antibodies, used for preventing and
PT treating urinary tract infections and cancer.
XX
PS Claim 1; Fig 1A-C; 113pp; English.
XX
XX This represents the consensus nucleotide sequence of the Utl16 gene. The
CC invention relates to a method of detecting the presence of a target Utl16
CC polynucleotide in a test sample using Utl16-specific sequences (AAV80386
CC to AAV80397). Host cells transfected with an expression vector containing
CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
CC This polypeptide has at least one Utl16 epitope which can be used in a
CC method for detecting Utl16 antigen in a test sample. The polynucleotides
CC and polypeptides are useful for detecting, diagnosing, monitoring,
CC staging, prognosticating, in vivo imaging, preventing, treating or
CC determining the predisposition of a subject to diseases and conditions of
CC the urinary tract, such as urinary tract cancer. Antibodies specifically
CC binding to an epitope of Utl16 antigen, and agonists are useful for
CC treating urinary tract diseases, tumours and metastases
XX
SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;
Query Match 100.0%; Score 293; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 9.8e-63;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGCCCTCTCCACCACAGCCACCCAGTCAGCATGACCATGAAGGCTGTGCTTGCCTGTGA 60
DB 26 GAGGCCCTCTCCACCACAGCCACCCAGTCAGCATGACCATGAAGGCTGTGCTTGCCTGTGA 85
QY 61 TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGTGCTTGCCTGTGA 120
DB 86 TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGTGCTTGCCTGTGA 145
QY 121 TGAGCAACGAGGACTGCTTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGA 180
DB 146 TGAGCAACGAGGACTGCTTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGA 205
QY 181 CCGCGCGCATCCGCGCAGTGGCCCTCTGACCGTATCATGCAAAAGGCTGCAGTTGA 240
DB 206 CCGCGCGCATCCGCGCAGTGGCCCTCTGACCGTATCATGCAAAAGGCTGCAGTTGA 265
QY 241 GCGTGGATGACTACAGGACTACTAGTGGGCAAGAGAACATCATCAGTCTGT 293
DB 266 GCGTGGATGACTACAGGACTACTAGTGGGCAAGAGAACATCATCAGTCTGT 318
RESULT 4
AAV68613
ID AAV68613 standard; cDNA; 1023 BP.
XX
XX AAV68613;
XX
XX 16-MAR-1999 (first entry)
XX
XX Human PS116 EST clone 1543671H.
XX
XX Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
XX detection; therapy; prostate cancer; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WC9851805-A1.
XX
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PD 19-NOV-1998.
XX
XX 15-MAY-1998; 98WO-US010041.
XX
XX 15-MAY-1997; 97US-00856653.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
XX WPI; 1999-045234/04.
XX
XX New method for detecting diseases of the prostate - comprises use of a
PT PS116 polynucleotide, protein or antibodies, useful for preventing and
PT treating prostate infections and cancer.
XX
PS Claim 1; Page 94; 118pp; English.
XX
XX This sequence represents an expressed sequence tag (EST) clone of the
CC PS116 gene isolated from a human prostate tissue library. This sequence
CC can be used in the method of the invention for detecting a target PS116
CC polynucleotide (PN), that comprises; contacting a sample with at least 1
CC PS116-specific PN or complement; and detecting the target PS116 PN, where
CC the specific PN has at least 50% identity with this sequence. The PNs,
CC PS116 polypeptides or PS116 amplicons are used to detect prostate
CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
CC solid phase. The polypeptides are used for detecting PS116-specific Abs
CC in a sample, and for producing Abs after immunising a subject. Plasmids
CC encoding PS116 epitopes can also be administered to a subject to obtain
CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC treating or determining the predisposition of a subject to diseases and
CC conditions of the prostate, such as prostate cancer. The Abs and agonists
CC or inhibitors are useful for treating prostate diseases, tumours and
XX metastases
XX
SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;
Query Match 100.0%; Score 293; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 9.8e-63;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGCCCTCTCCACCACAGCCACCCAGTCAGCATGACCATGAAGGCTGTGCTTGCCTGTGA 60
DB 26 GAGGCCCTCTCCACCACAGCCACCCAGTCAGCATGACCATGAAGGCTGTGCTTGCCTGTGA 85
QY 61 TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGTGCTTGCCTGTGA 120
DB 86 TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGTGCTTGCCTGTGA 145
QY 121 TGAGCAACGAGGACTGCTTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGA 180
DB 146 TGAGCAACGAGGACTGCTTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGA 205
QY 181 CCGCGCGCATCCGCGCAGTGGCCCTCTGACCGTATCATGCAAAAGGCTGCAGTTGA 240
DB 206 CCGCGCGCATCCGCGCAGTGGCCCTCTGACCGTATCATGCAAAAGGCTGCAGTTGA 265
QY 241 GCGTGGATGACTACAGGACTACTAGTGGGCAAGAGAACATCATCAGTCTGT 293
DB 266 GCGTGGATGACTACAGGACTACTAGTGGGCAAGAGAACATCATCAGTCTGT 318
RESULT 5
AAV68614
ID AAV68614 standard; cDNA; 1023 BP.
XX
XX AAV68614;
XX
XX 16-MAR-1999 (first entry)
XX
XX
```

XX DE Human PS116 EST clone consensus sequence.

XX DE Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;

XX KW detection; therapy; prostate cancer; metastasis; ss.

XX OS Homo sapiens.

XX PN WO9851805-A1.

XX PD 19-NOV-1998.

XX PF 15-MAY-1998; 98WO-US010041.

XX PR 15-MAY-1997; 97US-00856653.

XX PS (ABBO) ABBOTT LAB.

XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

XX PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;

XX PI Russell JC, Stroupe SD;

XX DR WPI; 1999-045234/04.

XX PT New method for detecting diseases of the prostate - comprises use of a

XX PT PS116 polynucleotide, protein or antibodies, useful for preventing and

XX PT treating prostate infections and cancer.

XX PS Claim 1; Page 94; 118pp; English.

XX CC This sequence represents an expressed sequence tag (EST) clone of the

XX CC PS116 gene isolated from a human prostate tissue library. This sequence

XX CC can be used in the method of the invention for detecting a target PS116

XX CC polynucleotide (PN), that comprises: contacting a sample with at least 1

XX CC PS116-specific PN or complement; and detecting the target PS116 PN, where

XX CC the specific PN has at least 50% identity with this sequence. The PNs,

XX CC PS116 polypeptides or PS116 amplicons are used to detect prostate

XX CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect

XX CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a

XX CC solid phase. The polypeptides are used for detecting PS116-specific Abs

XX CC in a sample, and for producing Abs after immunising a subject. Plasmids

XX CC encoding PS116 epitopes can also be administered to a subject to obtain

XX CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,

XX CC staging, monitoring, prognosticating, in vivo imaging, preventing,

XX CC treating or determining the predisposition of a subject to diseases and

XX CC conditions of the prostate, such as prostate cancer. The Abs and agonists

XX CC or inhibitors are useful for treating prostate diseases, tumours and

XX CC metastases

XX SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;

Query Match 100.0%; Score 293; DB 2; Length 1023;

Best Local Similarity 100.0%; Pred. No. 9.8e-63;

Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGCCCTCTCCACACAGCCACAGTACCATGAGGCTGTGCTGTGCTGTGCTGTGA 60

DB 26 GAGGCCCTCTCCACACAGCCACAGTACCATGAGGCTGTGCTGTGCTGTGCTGTGA 85

QY 61 TGACAGGCTTGGCCCTGACAGCAGGACCTGCCCTGTGCTGTGCTGTGCTGTGCTGTGA 120

DB 86 TGACAGGCTTGGCCCTGACAGCAGGACCTGCCCTGTGCTGTGCTGTGCTGTGCTGTGA 145

QY 121 TGACAGCAGGAGTCCCTGACAGTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGA 180

DB 146 TGACAGCAGGAGTCCCTGACAGTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGA 205

QY 181 CCGCGCGCATCCCGCAGTGTGCTCTGACCGTATGACGAAAGGCTGACGTTGAACT 240

DB 206 CCGCGCGCATCCCGCAGTGTGCTCTGACCGTATGACGAAAGGCTGACGTTGAACT 265

QY 241 CGGTGATGACTACAGGACTACTAGTGGCAAGAGAACATCAGTGTGCTGT 293

DB 266 GCGTGGATGACTACAGGACTACTAGTGGCAAGAGAACATCAGTGTGCTGT 318

RESULT 6

ADE53926

ID ADE53926 standard; cDNA; 1028 BP.

XX AC ADE53926;

XX XX 29-JAN-2004 (first entry)

XX DE Human prostate cancer cDNA #273.

XX KW Human; prostate cancer; ss; cDNA combination; differential expression;

XX KW gene.

XX OS Homo sapiens.

XX PN US2003190640-A1.

XX PD 09-OCT-2003.

XX PF 29-MAY-2002; 2002US-00252157.

XX PR 31-MAY-2001; 2001US-0295048P.

XX PA (FARI/) FARIS M.

XX PA (PEAR/) PEARSON C I.

XX PI Faris M, Pearson CI;

XX DR WPI; 2003-831619/77.

XX PT New combination comprising cDNAs that are differentially expressed in

XX PT prostate cancer, useful for diagnosing, treating or monitoring the

XX PT progression of treatment of prostate cancer.

XX PS Claim 1; SEQ ID NO 273; 42pp; English.

XX CC The invention relates to a combination comprising a number of cDNAs

XX CC expressed in prostate cancer. The invention also relates to a method for

XX CC detecting differential expression of one or more cDNAs in a sample

XX CC containing nucleic acids by hybridising a substrate with the nucleic

XX CC acids, thus forming one or more hybridisation complexes, detecting

XX CC hybridisation complex formation and comparing the complexes formed with

XX CC standard complexes, where differences between the standard and the sample

XX CC complex formation indicate differential expression of cDNAs in the

XX CC sample. The differential expression is diagnostic of prostate cancer. The

XX CC invention also relates to proteins and antibodies related to the cDNAs.

XX CC The combination is useful for diagnosing, treating or monitoring the

XX CC progression of treatment of prostate cancer. The antibodies are useful

XX CC for detecting prostate cancer. This sequence represents a human prostate

XX CC cancer cDNA of the invention.

XX SQ Sequence 1028 BP; 199 A; 350 C; 288 G; 191 T; 0 U; 0 Other;

Query Match 100.0%; Score 293; DB 9; Length 1028;

Best Local Similarity 100.0%; Pred. No. 9.8e-63;

Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGCCCTCTCCACACAGCCACAGTACCATGAGGCTGTGCTGTGCTGTGCTGTGA 60

DB 26 GAGGCCCTCTCCACACAGCCACAGTACCATGAGGCTGTGCTGTGCTGTGCTGTGA 85

QY 61 TGACAGGCTTGGCCCTGACAGCAGGACCTGCCCTGTGCTGTGCTGTGCTGTGCTGTGA 120

DB 86 TGACAGGCTTGGCCCTGACAGCAGGACCTGCCCTGTGCTGTGCTGTGCTGTGCTGTGA 145

QY 121 TGACAGCAGGAGTCCCTGACAGTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGA 180

DB 146 TGACAGCAGGAGTCCCTGACAGTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGA 205

QY 181 CCGCGCGCATCCCGCAGTGTGCTCTGACCGTATGACGAAAGGCTGACGTTGAACT 240

Query Match 98.9%; Score 289.8; DB 3; Length 373;
 Best Local Similarity 98.3%; Pred. No. 4.9e-62;
 Matches 288; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGCGCTCTCCACACACACCCACAGTACCATGAAGGCTGTGCTTGGCCCTGTGA 60
 DB 77 GAGGCGCTCTCCACACACACCCACAGTACCATGAAGGCTGTGCTTGGCCCTGTGA 136
 QY 61 TGGCAGGCTTGGCCCTTGACGAGCAGCACTGGCCCTGTGCTTACTCTCTGCAAGCCAGG 120
 DB 137 TGGCAGGCTTGGCCCTTGACGAGCAGCACTGGCCCTGTGCTTACTCTCTGCAAGCCAGG 196
 QY 121 TGAGCAAGAGAGACTGCTCTGAGTGGAGTGAAGTACGACCCAGCTGGGGAGAGTGTGGA 180
 DB 197 TGRGAACAGAGAGACTGCTCTGAGTGGAGTGAAGTACGACCCAGCTGGGGAGAGTGTGGA 256
 QY 181 CCGCGCGATCCGCGCAGTGGCCCTCTGACCGTCTATCAGCAAAAGGCTGACGCTTGAAC 240
 DB 257 CCGCGCGATCCGCGCAGTGGCCCTCTGACCGTCTATCAGCAAAAGGCTGACGCTTGAAC 316
 QY 241 GCGTGGATGATCAGAGCACTACTACGTGGGCAAGAAACATCAGCTGTGT 293
 DB 317 GCGTGGATGATCAGAGCACTACTACGTGGGCAAGAAACATCAGCTGTGT 369

RESULT 9

AAV80388
 ID AAX36801 standard; DNA; 979 BP.

XX AC AAX36801;
 XX AC AAX36801;

DT 14-JUL-1999 (first entry)

DE Human transmembrane protein coding sequence, HP01244.

XX Transmembrane protein; human; cell membrane; proliferation; diagnosis;
 KW cell differentiation; carcinostatic agent; probe; gene therapy;
 KW signal transduction; apoptosis; inhibitor;
 KW phosphatidylethanolamine N-methyltransferase; ss.

XX Homo sapiens.

XX WO9918203-A2.

XX 15-APR-1999.

XX 05-OCT-1998; 98WO-JP004475.

XX 08-OCT-1997; 97JP-00276271.

XX (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Yamaguchi T, Sekine S, Kobayashi M;

XX WPI; 1999-277268/23.

XX P-PSDB; AAY13938.

XX Human transmembrane proteins and nucleotide sequences.

XX Claim 4; Page 104-105; 139pp; English.

XX This sequence encodes a human transmembrane protein of the invention. All
 CC of the proteins exist in the cell membrane, so are considered to be
 CC proteins controlling the proliferation and differentiation of the cells.
 CC They may be useful as carcinostatic agents or as antigens for preparing
 CC antibodies against the proteins. The cDNAs can be used as probes for gene
 CC diagnosis and gene sources for gene therapy, as well as for large-scale
 CC expression of the proteins. The HP01498 (see AAY13939) protein may be
 CC associated with signal transduction associated with apoptosis, and
 CC therefore useful in inhibition of apoptosis. The HP01962 (see AAY13943)
 CC protein can be used to treat diseases associated with
 CC phosphatidylethanolamine N-methyltransferase. The proteins are identified

CC by the presence of a hydrophobic transmembrane region, knowledge of the
 CC protein function is not required, as in e.g. methods of expression
 CC cloning

XX Sequence 979 BP; 183 A; 334 C; 280 G; 182 T; 0 U; 0 Other;

Query Match 93.7%; Score 274.4; DB 2; Length 979;
 Best Local Similarity 99.6%; Pred. No. 3.7e-58;

Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 AGCCACCACTGACCATGAAGGCTGTGCTTGGCCCTGTGCTTGGCCCTGTGCTTGGCCCTGTG 77
 DB 1 AGCCACCACTGACCATGAAGGCTGTGCTTGGCCCTGTGCTTGGCCCTGTGCTTGGCCCTGTG 60

QY 78 GAGCCAGGCACTGCCCTGTGCTTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 137
 DB 61 GAGCCAGGCACTGCCCTGTGCTTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 120

QY 138 CTGCAGGTGGAGAACTGCAACCCAGCTGGGGAGAGTGTGACCCGGCATCCGCCCA 197
 DB 121 CTGCAGGTGAAGAACTGCAACCCAGCTGGGGAGAGTGTGACCCGGCATCCGCCCA 180

QY 198 GTTGGCTCTCTGACCGTCTATCAGCAAGGCTGCACTTGAACCTGCTGATCACTCAG 257
 DB 181 GTTGGCTCTCTGACCGTCTATCAGCAAGGCTGCACTTGAACCTGCTGATCACTCAG 240

QY 258 GACTACTAGTGGGCAAGAAACATCAGCTGTGT 293
 DB 241 GACTACTAGTGGGCAAGAAACATCAGCTGTGT 276

DE Nucleotide sequence of UT116 gene-specific clone 1891065.

XX UT116; urinary tract; epitope; antigen; detection; diagnosing;
 KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
 KW metastasis; ss.

XX Homo sapiens.

XX WO9851824-A1.

XX 19-NOV-1998.

XX 15-MAY-1998; 98WO-US009972.

XX 15-MAY-1997; 97US-00856652.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman FN, Granados EN;
 PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
 PI Stroupe SD;

XX WPI; 1999-045237/04.

XX New method for detecting diseases of the urinary tract - comprises use of
 CC a UT116 polynucleotide, protein or antibodies, used for preventing and
 CC treating urinary tract infections and cancer.

XX Claim 1; Fig 1A-C; 113pp; English.

XX Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
 CC sequences of the UT116 gene-specific clones derived from urinary tract
 CC tissue. The invention relates to a method of detecting the presence of a
 CC target UT116 polynucleotide in a test sample using these UT116-specific

CC sequences. Host cells transfected with an expression vector containing
CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
CC This polypeptide has at least one Utl16 epitope which can be used in a
CC method for detecting Utl16 antigen in a test sample. The polynucleotides
CC and polypeptides are useful for detecting, diagnosing, monitoring,
CC staging, prognosticating, in vivo imaging, preventing, treating or
CC determining the predisposition of a subject to diseases and conditions of
CC the urinary tract, such as urinary tract cancer. Antibodies specifically
CC binding to an epitope of Utl16 antigen, and agonists are useful for
CC treating urinary tract diseases, tumours and metastases
XX

XX Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;

Query Match 91.8%; Score 269; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 84
DB 1 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 60

QY 85 GCACCTGCCCTGCTGTCTACTCTCCGAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 144
DB 61 GCACCTGCCCTGCTGTCTACTCTCTGAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 120

QY 145 TGGAGAACTGCACCCAGCTGGGGAGGAGTCTGGACCGCGCGCATCCGGCGAGTTGGCC 204
DB 121 TGGAGAACTGCACCCAGCTGGGGAGGAGTCTGGACCGCGCGCATCCGGCGAGTTGGCC 180

QY 205 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCACAGGACTACT 264
DB 181 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCACAGGACTACT 240

QY 265 ACGTGGGCAAGAAGCAATCATCGTGTCT 293

DB 241 ACGTGGGCAAGAAGCAATCATCGTGTCT 269

RESULT 11

AAV68605
ID AAV68605 standard; cDNA; 279 BP.

AC AAV68605;

XX 16-MAR-1999 (first entry)

XX Human PS116 EST clone 1891065.

DE Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
KW detection; therapy; prostate cancer; metastasis; ss.

XX Homo sapiens.

OS WO9851805-A1.

PN 19-NOV-1998.

XX 15-MAY-1998; 98WO-US010041.

PF 15-MAY-1997; 97US-00856653.

PR (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;

PI Russell JC, Stroupe SD;

XX WPI; 1999-045234/04.

DR New method for detecting diseases of the prostate - comprises use of a
PT PS116 polynucleotide, protein or antibodies, useful for preventing and
PT treating prostate infections and cancer.

XX

PS Claim 1; Page 92; 118pp; English.

XX This sequence represents an expressed sequence tag (EST) clone of the
CC PS116 gene isolated from a human prostate tissue library. This sequence
CC can be used in the method of the invention for detecting a target PS116
CC polynucleotide (PN), that comprises: contacting a sample with at least 1
CC PS116-specific PN or complement; and detecting the target PS116 PN, where
CC the specific PN has at least 50% identity with this sequence. The PNs,
CC PS116 polypeptides or PS116 amplicons are used to detect prostate
CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
CC solid phase. The polypeptides are used for detecting PS116-specific Abs
CC in a sample, and for producing Abs after immunising a subject. Plasmids
CC encoding PS116 epitopes can also be administered to a subject to obtain
CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC treating or determining the predisposition of a subject to diseases and
CC conditions of the prostate, such as prostate cancer. The Abs and agonists
CC or inhibitors are useful for treating prostate diseases, tumours and
CC metastases

XX Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;

Query Match 91.8%; Score 269; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 6.3e-57;

Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 84

DB 1 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 60

QY 85 GCACCTGCCCTGCTGTCTACTCTCCAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 144

DB 61 GCACCTGCCCTGCTGTCTACTCTCTGAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 120

QY 145 TGGAGAACTGCACCCAGCTGGGGAGGAGTCTGGACCGCGCGCATCCGGCGAGTTGGCC 204

DB 121 TGGAGAACTGCACCCAGCTGGGGAGGAGTCTGGACCGCGCGCATCCGGCGAGTTGGCC 180

QY 205 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCACAGGACTACT 264

DB 181 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCACAGGACTACT 240

QY 265 ACGTGGGCAAGAAGCAATCATCGTGTCT 293

DB 241 ACGTGGGCAAGAAGCAATCATCGTGTCT 269

RESULT 12

ACCS1040

ID ACCS1040 standard; cDNA; 990 BP.

XX ACCS1040;

XX 12-JUN-2003 (first entry)

DE Human bladder cancer associated cDNA sequence SEQ ID NO:168.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.

OS Homo sapiens.

XX WO2003003905-A2.

PN 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021338.

XX 03-JUL-2001; 2001US-0302814P.

PR 03-AUG-2001; 2001US-0310099P.

PR 08-NOV-2001; 2001US-0343705P.

PR 13-NOV-2001; 2001US-0350666P.

PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Mack DH, Aziz N;
 PI WPI; 2003-201532/19.
 DR P-PSDB; ABR48224.
 XX
 PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 PS
 PS Claim 6; Page 289; 307pp; English.
 XX
 XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridizes to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications
 XX
 SQ Sequence 990 BP; 193 A; 299 C; 285 G; 202 T; 0 U; 11 Other;
 Query Match 91.8%; Score 269; DB 7; Length 990;
 Best Local Similarity 100.0%; Pred. No. 8.1e-57;
 Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 CAGTGACCATCAAGGCTGTGCTGCTTGGCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 84
 DB 10 CAGTGACCATCAAGGCTGTGCTGCTTGGCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 69
 QY 85 GCATGCGCCCTGTGTGCTTACTCTCTGCAAGCCAGGCTGAGCAAGAGATGTGCTGCAGG 144
 DB 70 GCATGCGCCCTGTGTGCTTACTCTCTGCAAGCCAGGCTGAGCAAGAGATGTGCTGCAGG 129
 QY 145 TGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCGCGCGCATCCGCGCAGTTGGCC 204
 DB 130 TGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCGCGCGCATCCGCGCAGTTGGCC 189
 QY 205 TCCTGACCGTTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGGATGACTCAGAGACTACT 264
 DB 190 TCCTGACCGTTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGGATGACTCAGAGACTACT 249
 QY 265 ACGTGGGCAAGAAGACATCAGTGTCTGT 293
 DB 250 ACGTGGGCAAGAAGACATCAGTGTCTGT 278
 RESULT 13
 ABR48383
 ID ABR48383 standard; cDNA; 990 BP.
 XX
 AC ABR48383;
 XX
 DT 03-FEB-2003 (first entry)
 XX
 DE Human PSCA encoding cDNA SEQ ID NO:87.
 XX
 XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
 KW T cell; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200201646-A2.

XX 17-OCT-2002.
 XX 04-APR-2002; 2002WO-US011101.
 XX 06-APR-2001; 2001US-0282211P.
 PR 07-NOV-2001; 2001US-0337017P.
 PR 07-MAR-2002; 2002US-0363210P.
 XX
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Simard JLL, Diamond DC, Liu L, Xie Z;
 XX WPI; 2003-067518/06.
 DR P-PSDB; ABR74203.
 XX
 PT Novel epitopes useful as vaccines, comprises peptides or nucleic acid
 PT encoding the peptides, that are useful epitopes of target-associated
 PT antigens.
 XX
 PS Claim 1; Page 164-165; 352pp; English.
 XX
 CC The present invention describes an isolated epitope (I) and an epitope
 CC cluster. Also described is a vaccine or immunotherapeutic composition
 CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
 CC treating an animal, by administering to an animal the vaccine or
 CC immunotherapeutic composition. VC is also useful for evaluating
 CC immunogenicity of a vaccine or immunotherapeutic composition, by
 CC administering VC to an HLA-transgenic animal and evaluating
 CC immunogenicity based on a characteristic of the animal, or by in vitro
 CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
 CC useful for determining specific T cell frequency, by contacting T cells
 CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
 CC limiting dilution analysis, flow cytometry, in situ hybridisation, and/or
 CC polymerase chain reaction (PCR). ABR83843 to ABR83858 and ABR74128 to
 CC ABR74713 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 990 BP; 193 A; 299 C; 285 G; 202 T; 0 U; 11 Other;
 Query Match 91.8%; Score 269; DB 7; Length 990;
 Best Local Similarity 100.0%; Pred. No. 8.1e-57;
 Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 CAGTGACCATCAAGGCTGTGCTGCTTGGCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 84
 DB 10 CAGTGACCATCAAGGCTGTGCTGCTTGGCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 69
 QY 85 GCATGCGCCCTGTGTGCTTACTCTCTGCAAGCCAGGCTGAGCAAGAGACTGCTGCAGG 144
 DB 70 GCATGCGCCCTGTGTGCTTACTCTCTGCAAGCCAGGCTGAGCAAGAGACTGCTGCAGG 129
 QY 145 TGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCGCGCGCATCCGCGCAGTTGGCC 204
 DB 130 TGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCGCGCGCATCCGCGCAGTTGGCC 189
 QY 205 TCCTGACCGTTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGGATGACTCAGAGACTACT 264
 DB 190 TCCTGACCGTTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGGATGACTCAGAGACTACT 249
 QY 265 ACGTGGGCAAGAAGACATCAGTGTCTGT 293
 DB 250 ACGTGGGCAAGAAGACATCAGTGTCTGT 278
 RESULT 14
 ADC09589
 ID ADC09589 standard; DNA; 990 BP.
 XX
 AC ADC09589;
 XX
 DT 18-DEC-2003 (first entry)
 XX

CC compounds, assist in identification of rare genes associated with
 CC prostate cancer, and to isolate and purify PSA and PSCA homologues. The
 CC present nucleic acid sequence encodes the human prostate stem cell
 CC antigen (PSCA) protein of the invention
 XX
 SQ Sequence 998 BP; 201 A; 299 C; 285 G; 202 T; 0 U; 11 Other;
 Query Match 91.8%; Score 269; DB 4; Length 998;
 Best Local Similarity 100.0%; Pred.No. 8.1e-57;
 Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 CAGTGACCATGAAGCTGTGCTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAG 84
 DB 10 CAGTGACCATGAAGCTGTGCTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAG 69
 QY 85 GCATGGCCCTGCTGTGCTACTTCCTGCAAAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 144
 DB 70 GCATGGCCCTGCTGTGCTACTTCCTGCAAAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 129
 QY 145 TGGAGACTGCACCCAGCTGGGGGAGCAGTCTGGACCGCGGCATCCGCGCAGTTGGCC 204
 DB 130 TGGAGACTGCACCCAGCTGGGGGAGCAGTCTGGACCGCGGCATCCGCGCAGTTGGCC 189
 QY 205 TCCTGACCGTTCATCAGCAAAAGCTGCAGCTTGAACCTCGTGATGACTCACAGGACTACT 264
 DB 190 TCCTGACCGTTCATCAGCAAAAGCTGCAGCTTGAACCTCGTGATGACTCACAGGACTACT 249
 QY 265 ACGTGGGCAAGAGAACATCAGTGTCTGT 293
 DB 250 ACGTGGGCAAGAGAACATCAGTGTCTGT 278

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 Job time : 193.537 secs

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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 06:05:35 ; Search time 34.2284 Seconds
(without alignments)
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Perfect score: 293
Sequence: 1 GAGCCCTCTCCACACAGC.....AGAGAATCATCAGTCTGT 293

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	269	91.8	998	3	US-09-203-939-1
2	269	91.8	998	3	US-09-251-835-1
3	269	91.8	998	3	US-09-318-503-1
4	269	91.8	998	3	US-09-318-503-1
5	269	91.8	998	4	US-09-318-261A-1
6	267	91.1	288	2	US-08-675-508-23
7	267	91.1	494	2	US-08-675-508-4
8	250	85.3	960	4	US-09-907-794A-17
9	250	85.3	960	4	US-09-905-125A-17
10	250	85.3	960	4	US-09-902-775A-17
11	218	74.5	232	2	US-08-675-508-25
12	218	74.4	286	2	US-08-675-508-21
13	144.8	49.4	441	3	US-09-203-939-3
14	144.8	49.4	441	3	US-09-251-835-3
15	144.8	49.4	441	3	US-09-318-503-3
16	144.8	49.4	441	3	US-09-318-261A-3
17	144.8	49.4	441	4	US-09-564-329A-3
18	52.4	17.9	280	2	US-08-675-508-17
19	52.2	17.8	262	2	US-08-675-508-10
20	52.2	17.8	289	2	US-08-675-508-11
21	52.2	17.8	537	2	US-08-675-508-3
22	52.2	17.8	1066	1	US-08-154-916-1
23	52.2	17.8	1095	2	US-09-139-424-1
24	52.2	17.8	1163	3	US-08-746-397-1
25	51.2	17.5	266	2	US-08-675-508-16
26	51.2	17.5	335	2	US-08-675-508-12
27	46.8	16.0	196	2	US-08-675-508-8

28	44.4	15.2	275	2	US-08-675-508-18	Sequence 18, Appl
29	44	15.0	44	4	US-09-907-794A-21	Sequence 21, Appl
30	44	15.0	44	4	US-09-905-125A-21	Sequence 21, Appl
31	44	15.0	44	4	US-09-902-775A-21	Sequence 21, Appl
32	43.6	14.9	1893	4	US-09-252-991A-3131	Sequence 3131, Ap
33	43.6	14.9	2805	4	US-09-252-991A-2944	Sequence 2944, Ap
34	43	14.7	1491	4	US-09-252-991A-9935	Sequence 9935, Ap
35	43	14.7	1656	4	US-09-252-991A-9845	Sequence 9845, Ap
36	43	14.7	2007	4	US-09-252-991A-10141	Sequence 10141, A
37	43	14.7	5184	4	US-09-845-583A-9	Sequence 9, Appl
38	43	14.7	5184	4	US-09-561-709B-4	Sequence 4, Appl
39	42.6	14.5	261	2	US-08-675-508-13	Sequence 13, Appl
40	41.2	14.1	720	4	US-09-252-991A-3324	Sequence 3324, Ap
41	41.2	14.1	1191	4	US-09-252-991A-3242	Sequence 3242, Ap
42	38.8	13.2	903	4	US-09-252-991A-908	Sequence 908, App
43	38.8	13.2	1551	4	US-09-252-991A-1128	Sequence 1128, Ap
44	38.2	13.0	1554	4	US-09-252-991A-4893	Sequence 4893, Ap
45	38.2	13.0	2139	4	US-09-252-991A-4910	Sequence 4910, Ap

ALIGNMENTS

RESULT 1

US-09-203-939-1
; Sequence 1, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (590)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (615)
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; NAME/KEY: misc feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)


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/ EARLIER FILING DATE: 1999-02-17
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/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 998
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/ ORGANISM: HUMAN PSCA (hPSCA)
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: [543]
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ FEATURE:
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/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ NAME/KEY: misc_feature
/ LOCATION: [604]
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
/
/ FEATURE:
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/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: [926]
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ US-09-318-503-1

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Db	10	CAGTGNACATGAAGGCTGTGCTGTTGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAG	69		
Qy	85	GCAGTCCCTGCTGTGCTACTCTTGAAAGCCCAAGGTGAGCAACGAGGACTGCCTGCAGG	144		
Db	70	GCAGTCCCTGCTGTGCTACTCTTGAAAGCCCAAGGTGAGCAACGAGGACTGCCTGCAGG	129		
Qy	145	TGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGGACCGCGGCATCCGCGCAGATTGCC	204		
Db	130	TGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGGACCGCGGCATCCGCGCAGATTGCC	189		
Qy	205	TCTGACCGTCATCAGCAAAAGGCTGCAGCTTGAATCGCTTGGATGACTCACAGGACTACT	264		
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QY      25  ACGTGGCGAAGAGACATCACGTGCTGT 293
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Db      25  ACGTGGCGAAGAGACATCACGTGCTGT 278
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RESULT 4
US-09-038-261A-1
; Sequence 1, Application US/09038261A
; Patent No. 6267960
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54USU1
; CURRENT APPLICATION NUMBER: US/09/039,261A
; CURRENT FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-04-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998

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1 TYPE: DNA
2 ORGANISM: HUMAN PSCA (hPSCA)
3
4 FEATURE:
5 NAME/KEY: misc feature
6 LOCATION: {543}
7 OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
8
9 NAME/KEY: misc feature
10 LOCATION: {580}
11 OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
12
13 NAME/KEY: misc feature
14 LOCATION: {584}
15 OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
16
17 NAME/KEY: misc feature
18 LOCATION: {604}
19 OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
20
21 NAME/KEY: misc feature
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23 OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
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25 NAME/KEY: misc feature
26 LOCATION: {613}
27 OTHER INFORMATION: any nucleotide (i.e. a, c, g, or t)
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29 NAME/KEY: misc feature
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31 OTHER INFORMATION: any nucleotide (i.e. a, c, g, or t)
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33 NAME/KEY: misc feature
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35 OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
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37 NAME/KEY: misc feature
38 LOCATION: {646}
39 OTHER INFORMATION: any nucleotide (i.e. a, c, g, or t)
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41 NAME/KEY: misc feature
42 LOCATION: {697}
43 OTHER INFORMATION: any nucleotide (i.e. a, c, g, or t)
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45 NAME/KEY: misc feature
46 LOCATION: {926}
47 OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
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49 US-09-038-361A-1

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Query Match	91.8%	Score 269;	DB 3;	Length 398;
Best Local Similarity	100.0%;	Pred. NO. 8e-61;		
Matches 269;	Conservative	0;	Mismatches	0;
Indels				0;
Gaps				0;
Qy	25	CAGTGCACATGAAGCGTGTGCTGTGTTGCCCTTTGATGGCAGGCTTGCCCTGCAGCCAG	84	
Db	10	CAGTGCACATGAAGCGTGTGCTGTGTTGCCCTTTGATGGCAGGCTTGCCCTGCAGCCAG	69	
Ov	85	GCATCGCCCTGCTGTGCTACTCTCTGAAAGGCCAGGTGAGCAAGAGACTGCTCTGCAGG	144	

APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 17
LENGTH: 960
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-794A-17

Query Match 85.3%; Score 250; DB 4; Length 960;

Best Local Similarity 100.0%; Pred. No. 6.6e-56; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 GCTGTTCCCTGTGTGATGGCAGGCTTGGCCCTCGACCGAGGCACTGCCCTGTGTGCTA 103
Db 1 GCTGTTCCCTGTGTGATGGCAGGCTTGGCCCTCGACCGAGGCACTGCCCTGTGTGCTA 60
QY 104 CTCCTGCAAAAGCCAGGAGTGCACGAGGAGTGCCTGCTGAGTGCAGCACTGCCCCAGCT 163
Db 61 CTCCTGCAAAAGCCAGGAGTGCACGAGGAGTGCCTGCTGAGTGCAGCACTGCCCCAGCT 120
QY 164 GGGGAGCAGTGTGACCGCCGCGCATCCGCGCAGTGGCTCTCTGACCGTCTATCAGCAA 223
Db 121 GGGGAGCAGTGTGACCGCCGCGCATCCGCGCAGTGGCTCTCTGACCGTCTATCAGCAA 180
QY 224 AGGTCGACGTTGACCTCGTGGTGTACTACAGGACTACTACGTCGGGCAAGAGACAT 283
Db 181 AGGTCGACGTTGACCTCGTGGTGTACTACAGGACTACTACGTCGGGCAAGAGACAT 240
QY 284 CACGTGTGT 293
Db 241 CACGTGTGT 250

RESULT 9

US-09-905-125A-17
Sequence 17, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman

Query Match 85.3%; Score 250; DB 4; Length 960;

Best Local Similarity 100.0%; Pred. No. 6.6e-56; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 GCTGTTCCCTGTGTGATGGCAGGCTTGGCCCTCGACCGAGGCACTGCCCTGTGTGCTA 103
Db 1 GCTGTTCCCTGTGTGATGGCAGGCTTGGCCCTCGACCGAGGCACTGCCCTGTGTGCTA 60
QY 104 CTCCTGCAAAAGCCAGGAGTGCACGAGGAGTGCCTGCTGAGTGCAGCACTGCCCCAGCT 163

Db 61 CTCCTGCAAGCCAGGTGACCAACAGGAGCTGCTCAGGTGAGAACTGCACCCAGCT 120
Qy 164 GGGGAGCAGTGTGGACCGCGCATCCGGCGAGTTGGCCCTCTCTGACCGTCAATCAGCAA 223
Db 121 GGGGAGCAGTGTGGACCGCGCATCCGGCGAGTTGGCCCTCTCTGACCGTCAATCAGCAA 180
Qy 224 AGGCTGACAGTTGAACTCCGTGGATGACTCACAGAGCTTACTACGTGGGCAAGAAACAT 283
Db 181 AGGCTGACAGTTGAACTCCGTGGATGACTCACAGAGCTTACTACGTGGGCAAGAAACAT 240
Qy 284 CACGTGCTGT 293
Db 241 CACGTGCTGT 250

RESULT 10
US-09-902-775A-17
; Sequence 17, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-17
Query Match 85.3%; Score 250; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 6.6e-56;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 44 GCTGCTTGCCCTGTTGATGCGAGGCTTGGCCCTGCGAGGCACTGCGCCCTGCTGTGCTA 103
Db 1 GCTGCTTGCCCTGTTGATGCGAGGCTTGGCCCTGCGAGGCACTGCGCCCTGCTGTGCTA 60
Qy 104 CTCCTGCAAGCCAGGTGAGCAAACGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCT 163
Db 61 CTCCTGCAAGCCAGGTGAGCAAACGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCT 120
Qy 164 GGGGAGCAGTGTGGACCGCGCATCCGGCGAGTTGGCCCTCTCTGACCGTCAATCAGCAA 223
Db 121 GGGGAGCAGTGTGGACCGCGCATCCGGCGAGTTGGCCCTCTCTGACCGTCAATCAGCAA 180
Qy 224 AGGCTGACAGTTGAACTCCGTGGATGACTCACAGGACTTACTACGTGGGCAAGAAACAT 283
Db 181 AGGCTGACAGTTGAACTCCGTGGATGACTCACAGGACTTACTACGTGGGCAAGAAACAT 240
Qy 284 CACGTGCTGT 293
Db 241 CACGTGCTGT 250

RESULT 11
US-08-675-508-25
; Sequence 25, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0066 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT02
; CLONE: 1315052

US-08-675-508-25

Query Match 74.5%; Score 218.4; DB 2; Length 232;
Best Local Similarity 99.1%; Pred. No. 7.1e-48;
Matches 230; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 28 TGACCATGAAGGCTGTGCTTGGCTTGGCTTGGATGGCAGGCTTGGCCCTGCAGCCAGGCA 87
Db 1 TGACCATGAAGGCTGTGCTTGGCTTGGATGGCAGGCTTGGCCCTGCAGCCAGGCA 60
QY 88 CTGCCCTGTGTGTACTCTCTGCAAGCCAGGTGAGCAACGAGACTGTGCTGAGGTGG 147
Db 61 CTGCCCTGTGTGTACTCTCTGCAAGCCAGGTGAGCAACGAGACTGTGCTGAGGTGG 120
QY 148 AGAACTGCACCCAGCTGGGGGAGCAGTCTGACCGCGCGCATCCGGCAGTTCGCTCC 207
Db 121 AGAACTGCACCCAGCTGGGGGAGCAGTCTGACCGCGCGCATCCGGCAGTTCGCTCC 180
QY 208 TGACCGTGCATCAGC-AAAGGCTGCAGCTTGAATGCGTGGATGACTCACAGG 258
Db 181 TGACCGTGCATCAACAAAGGCTGCAGCTTGAATGCGTGGATGACTCACAGG 232

RESULT 12

US-08-675-508-21
; Sequence 21, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,508
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: UTRSN01
; CLONE: 588615

US-08-675-508-21

Query Match 74.4%; Score 218; DB 2; Length 286;
Best Local Similarity 97.9%; Pred. No. 9.5e-48;
Matches 229; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 60 ATGGCAGGCTTGGCCCTGCAGCAGGACTGCCCTGCTGTGCTACTCTGCAAGCCAG 119
Db 1 ATGGCAGGCTTGGCCCTGCAGCAGGACTGCCCTGCTGTGCTACTCTGCAAGCCAG 60
QY 120 GTGAGCAACGAGCACTGCTGTCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGG 179
Db 61 GTGAGCAACGAGCACTGCTGTCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGG 120
QY 180 ACCGGCGCATCCGGCAGTGTGGCTTCTGACCGTTCATCAGCAAGGCTGCAGCTTGAAC 239
Db 121 ACCGGCGCATTCG-CAAGTTGGCTTCTGACCGTTCATCAGCAAGGCTGCAGCTTGAAC 179
QY 240 TCGTGGATGACTCACAGGACTACTACGTGGGCAAGAGAAACATCACGTGTGT 293
Db 180 TCGTGGATGACTNACAGACTACTACGTGGGCAAGAGAAACATCACGTGTGT 233

RESULT 13

US-09-203-939-3
; Sequence 3, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)

US-09-203-939-3
Query Match 49.4%; Score 144.8; DB 3; Length 441;
Best Local Similarity 72.3%; Pred. No. 9.3e-29;
Matches 188; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 33 ATGAAGGCTGTGCTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCC 92
Db 1 ATGAAGACAGATTTTTTTTATCTGCTGCGCCACTTACTTAGCCCTGCATCCAGGTGCTCT 60
QY 93 CTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACAGGACTGCTTCAGGTGGAGAAC 152
Db 61 CTGCACTGCTATTTCATGCACAGCAGATGAACACAGAGACTGTCTGAATGTACAGAAC 120
QY 153 TGCACCCAGCTGGGGAGAGTGTGGACCGCGCGCATCCGGCAGTGTGGCTCTCTGACC 212
Db 121 TGCAGCCTGGACCAAGTGTGCTTTTACATGGCGCATCCGGGCAATTTGACTCGTGACA 180
QY 213 GTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGGATGACTCACAGGACTACTACTGTGGGC 272
Db 181 GTTATCAGTAAGGCTTGAGCTCACAGTGTGAGGATGACTCGGAGAACTACTATTGGGC 240
QY 273 AAGAAGAACATCACGTGTG 292
Db 241 AAGAAGAACATCACGTGTG 260

US-09-251-835-3
; Sequence 3, Application US/09251835A
; Patent No. 6261789
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US12
; CURRENT APPLICATION NUMBER: US/09/251.835A
; PRIORITY FILING DATE: 1999-02-17
; PRIORITY FILING DATE: 08/814,279
; PRIORITY FILING DATE: 1997-03-10
; PRIORITY FILING DATE: 60/071,141
; PRIORITY FILING DATE: 1998-01-12
; PRIORITY FILING DATE: 60/074,675
; PRIORITY FILING DATE: 1998-02-13
; PRIORITY FILING DATE: 09/038,261
; PRIORITY FILING DATE: 1998-03-10
; PRIORITY FILING DATE: 09/203,939
; PRIORITY FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)
US-09-318-503-3
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)
US-09-318-503-3
Query Match 49.4%; Score 144.8; DB 3; Length 441;
Best Local Similarity 72.3%; Pred. No. 9.3e-29;
Matches 188; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 33 ATGAAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCC 92
Db 1 ATGAAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 93 CTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGGTGGAGAAC 152
Db 61 CTGCAGTGTCTATTTCATGTCACGACAGATGAACACAGAGACTGCTGTAATGTACAGAAC 120
QY 153 TGCACCCAGCTGGGGAGCAGTGTGGACCGCGCCGATCCGCGCAGTTGGCTTCTCTGACC 212
Db 121 TGCAGCTGGACCCAGCAGTGTGCTTACATCGCGCATCCGGGCCATTGGACTCTGTGACA 180
QY 213 GTCATCAGCAAGGCTGCGAGCTTGAACCTGCTGGATGACTCAGAGGACTACTACGTTGGGC 272
Db 181 GTTATCAGTAAGGGCTGCGAGCTCAGCTCAGTGTGAGGATGACTCGGAGAACTACTATTTTGGGC 240
QY 273 AAGAAGAACATCAGCTGCTG 292
Db 241 AAGAAGAACATCAGCTGCTG 260

Search completed: September 18, 2004, 19:23:17
Job time : 34.2284 secs

US-09-251-835-3
Query Match 49.4%; Score 144.8; DB 3; Length 441;
Best Local Similarity 72.3%; Pred. No. 9.3e-29;
Matches 188; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 33 ATGAAGGCTGTGCTGCTTGGCCCTGTGTGATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCC 92
Db 1 ATGAAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 93 CTGCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGGTGGAGAAC 152
Db 61 CTGCAGTGTCTATTTCATGTCACGACAGATGAACACAGAGACTGCTGTAATGTACAGAAC 120
QY 153 TGCACCCAGCTGGGGAGCAGTGTGGACCGCGCCGATCCGCGCAGTTGGCTTCTCTGACC 212
Db 121 TGCAGCTGGACCCAGCAGTGTGCTTACATCGCGCATCCGGGCCATTGGACTCTGTGACA 180
QY 213 GTCATCAGCAAGGCTGCGAGCTTGAACCTGCTGGATGACTCAGAGGACTACTACGTTGGGC 272
Db 181 GTTATCAGTAAGGGCTGCGAGCTCAGCTCAGTGTGAGGATGACTCGGAGAACTACTATTTTGGGC 240
QY 273 AAGAAGAACATCAGCTGCTG 292
Db 241 AAGAAGAACATCAGCTGCTG 260

RESULT 15
US-09-318-503-3
; Sequence 3, Application US/09318503A
; Patent No. 6261791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318,503A
; PRIORITY FILING DATE: 1999-05-25
; PRIORITY FILING DATE: 08/814,279
; PRIORITY FILING DATE: 1997-03-10
; PRIORITY FILING DATE: 60/071,141
; PRIORITY FILING DATE: 1998-01-12
; PRIORITY FILING DATE: 60/074,675
; PRIORITY FILING DATE: 1998-02-13

Blank sheet

QY 205 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAAGTGGTGGATGACTACAGGACTACT 264
DB 190 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAAGTGGTGGATGACTACAGGACTACT 249
QY 265 ACGTGGGCAAGAAGAACATCATCGTGTGT 293
DB 250 ACGTGGGCAAGAAGAACATCATCGTGTGT 278

RESULT 8

US-10-188-832-168
Sequence 168, Application US/10198832
Publication No. US20040076955A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 168
LENGTH: 990
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (1)-(990)
OTHER INFORMATION: n = g, a, c or t
US-10-188-832-168

Query Match 91.8%; Score 269; DB 17; Length 990;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CAGTGACCATGAAGCTGTGCTTGGCCCTGTTGATGCGAGGCTTGCCCTGCAGCCAG 84
DB 10 CAGTGACCATGAAGCTGTGCTTGGCCCTGTTGATGCGAGGCTTGCCCTGCAGCCAG 69
QY 85 GCACTGCCCTGTGCTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 144
DB 70 GCACTGCCCTGTGCTGCTACTCTCTCAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 129
QY 145 TGGAGAACTGACACCGAGTGGGAGAGAGTGTGACCGCGCGGATCCGCGAGTTGCC 204
DB 130 TGGAGAACTGACACCGAGTGGGAGAGAGTGTGACCGCGCGGATCCGCGAGTTGCC 189
QY 205 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAAGTGGTGGATGACTACAGGACTACT 264
DB 190 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAAGTGGTGGATGACTACAGGACTACT 249
QY 265 ACGTGGGCAAGAAGAACATCATCGTGTGT 293
DB 250 ACGTGGGCAAGAAGAACATCATCGTGTGT 278

RESULT 9

US-09-564-329A-1

Sequence 1, Application US/09564329A
Patent No. US20010055751A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saifran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/564,329A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 998
TYPE: DNA
ORGANISM: HUMAN PSCA (hPSCA)
FEATURE:
NAME/KEY: misc feature
LOCATION: (543)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (580)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (584)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (604)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (608)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (615)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (636)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (640)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (646)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (697)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (926)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-564-329A-1

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Query Match      91.8%; Score 269; DB 9; Length 998;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CAGTGACCATGAAGCTGTGCTGCTTCCCTGTTGATGCGCAGGCTTGGCCCTGCAGCCAG 84
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Db 10 CAGTGACCATGAAGCTGTGCTGCTTCCCTGTTGATGCGCAGGCTTGGCCCTGCAGCCAG 69
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QY 85 GCACCTGCCCTGCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 144
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QY 205 TCCTGACCGTCTATCAGCAAGGCTGCACTTGAAGTGGTGGATGACTCAAGGACTACT 264
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QY 265 ACCTGGGCAAGAAGAACATCACTGCTGT 293
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RESULT 10
US-09-855-153-1
; Sequence 1, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855.153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature

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Query Match      91.8%; Score 269; DB 9; Length 998;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CAGTGACCATGAAGCTGTGCTGCTTCCCTGTTGATGCGCAGGCTTGGCCCTGCAGCCAG 84
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Db 10 CAGTGACCATGAAGCTGTGCTGCTTCCCTGTTGATGCGCAGGCTTGGCCCTGCAGCCAG 69
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QY 85 GCACCTGCCCTGCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 144
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Db 70 GCACCTGCCCTGCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 129
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QY 145 TGGAGAACTGACCCAGCTGGGGGAGAGTCTCTGGACCGCGCGCATCCGGCAGTTGGCC 204
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QY 205 TCCTGACCGTCTATCAGCAAGGCTGCACTTGAAGTGGTGGATGACTCAAGGACTACT 264
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QY 265 ACCTGGGCAAGAAGAACATCACTGCTGT 293
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Db 250 ACCTGGGCAAGAAGAACATCACTGCTGT 278
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RESULT 11
US-09-854-811-1
; Sequence 1, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; US-09-854-811-1

Query Match          91.8%; Score 269; DB 9; Length 998;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGCGAGGCTTGCCCTTGAGCCAG 84
DB 10 CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGCGAGGCTTGCCCTTGAGCCAG 69
QY 85 GCACCTGCCCTGTGTGCTTACTCCTGCAAGCCAGGTCAGCAAGGACTGCTGCAGG 144
DB 70 GCACCTGCCCTGTGTGCTTACTCCTGCAAGCCAGGTCAGCAAGGACTGCTGCAGG 129
QY 145 TGGAGAACTGCCACCGAGTGGGGAGCAGTGTGACCCGCGCATCCGCGCACTTGCC 204
DB 130 TGGAGAACTGCCACCGAGTGGGGAGCAGTGTGACCCGCGCATCCGCGCACTTGCC 189
QY 205 TCCTGACCGTCTATCAGCAAGGCTCAGCTTGAAGTGGTGTGATCAGCAAGGACTT 264
DB 190 TCCTGACCGTCTATCAGCAAGGCTCAGCTTGAAGTGGTGTGATCAGCAAGGACTT 249
QY 265 ACGTGGGCAAGGAACATCAGTGTCTGT 293
DB 250 ACGTGGGCAAGGAACATCAGTGTCTGT 278

RESULT 12
US-09-934-773-1
; Sequence 1, Application US/09934773
; Patent No. US20020136689A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USBS THEREOF
; FILE REFERENCE: 30435.5AUS14
; CURRENT APPLICATION NUMBER: US/09/934,773
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; US-09-934-773-1

Query Match          91.8%; Score 269; DB 9; Length 998;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 269; Conservative 100.0%; Pred. No. 1.6e-70;

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Db	10	CAGTGACCATGAAGGCTGTGCTGCTTGCCCTGTTGATGTCAGGCTTGCCCTGCAGCCAG	69						
QY	85	GCACGTGCCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG	144						
Db	70	GCACGTGCCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG	129						
QY	145	TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGCCC	204						
Db	130	TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGCCC	189						
QY	205	TCTTCACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGCCGTGGATGACTCACAGGACTACT	264						
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QY	265	ACGTGGGCAAGAAGAACATCATCGTCTGT	293						
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RESULT 13

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US-09-963-620-1
; Sequence 1, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature

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RESULT 14

US-09-855-632-1
; Sequence 1, Application US/09855632
; Publication NO. US20030113818A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.5AUS14
; CURRENT APPLICATION NUMBER: US/09/855.632
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12

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	PRIOR FILING DATE: 1998-02-13	
	PRIOR APPLICATION NUMBER: 60/113,230	
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	PRIOR APPLICATION NUMBER: 60/120,536	
	PRIOR FILING DATE: 1999-02-17	
	PRIOR APPLICATION NUMBER: 60/124,658	
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	PRIOR APPLICATION NUMBER: 09/203,939	
	PRIOR FILING DATE: 1998-12-02	
	PRIOR APPLICATION NUMBER: 09/251,835	
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	PRIOR APPLICATION NUMBER: 09/308,503	
	PRIOR FILING DATE: 1999-05-25	
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	NAME/KEY: misc feature	
	LOCATION: (543)	
	OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)	
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	OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)	
	NAME/KEY: misc feature	
	LOCATION: (594)	
	OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)	
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	LOCATION: (615)	
	OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)	
	NAME/KEY: misc feature	
	LOCATION: (636)	
	OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)	
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	LOCATION: (640)	
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	NAME/KEY: misc feature	
	LOCATION: (646)	
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	Best Local Similarity 100.0%; Pred. No. 1.6e-70;	
	Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	25 CAGTGACCATGAGGTGGTCTGCTTCCTGTTGATGCAGGCTTGCCCTGCGCAG 84	
Dd	10 CAGTGACCATGAGGTGGTCTGCTTCCTGTTGATGCAGGCTTGCCCTGCGCAG 69	
Qy	85 GCAGTCCCTGCTGCTACTCTCTGAAGGCCAGGTGAGCAACGAGGACTCCCTGCGAG 144	
Dd	70 GCAGTCCCTGCTGCTACTCTCTGAAGGCCAGGTGAGCAACGAGGACTCCCTGCGAG 129	
Qy	145 TGAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCCGGCGCATCCCGCAGTTGGCC 204	
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Mon Sep 20 09:12:06 2004

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US-10-225-784-1

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QY      25 CAGTGACCATGAAGGCTGTGCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAG 84
Db      10 CAGTGACCATGAAGGCTGTGCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAG 69

QY      85 GCACCTGCCCTGCTGTGCTACTCCTGCAAGCCAGGTGAGCAAGAGACTGCCTGCAGG 144
Db      70 GCACCTGCCCTGCTGTGCTACTCCTGCAAGCCAGGTGAGCAAGAGACTGCCTGCAGG 129

QY      145 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGTGACCCGCCGATCCGGCAGTTGGCC 204
Db      130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGTGACCCGCCGATCCGGCAGTTGGCC 189

QY      205 TCCTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 264
Db      190 TCCTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 249

QY      265 ACGTGGCAAGAAGAACATCAGTCTGT 293
Db      250 ACGTGGCAAGAAGAACATCAGTCTGT 278

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Search completed: September 18, 2004, 20:20:19
Job time : 219.589 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 05:54:35 ; Search time 1339.86 Seconds
(without alignments)
6530.246 Million cell updates/sec

Title: US-09-079-874-2
Perfect score: 293
Sequence: 1 GAGGCCCTCTCCACCACAGC.....AGAGAACAATCAGCTGCTGT 293

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

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6: em_estpl:*

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9: gb_est1:*

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17: em_gss_hum:*

18: em_gss_inv:*

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22: em_gss_nam:*

23: em_gss_mus:*

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29: gb_gss2:*

SUMMARIES

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2	293	100.0	470	13	BQ083505
3	293	100.0	527	13	BQ083498
4	291.4	99.5	843	14	CB997275

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	291.4	99.5	851	14	CB993163
6	278	94.9	480	12	BM819937
7	278	94.9	550	14	CB147558
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12	272.8	93.1	315	12	BM750435
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43	148	50.5	861	11	AK008851
44	147.8	50.4	1025	13	BQ230697
45	147	50.2	355	13	BY084639

ALIGNMENTS

RESULT 1
BM768967
LOCUS
DEFINITION K-EST0052116 S14K402 Homo sapiens cdna clone S14K402-13-D04 5',
424 bp mRNA linear EST 04-MAR-2002
mRNA sequence.
ACCESSION BM768967
VERSION BM768967.1 GI:19098582
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 424)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 13 row: D column: 04
High quality sequence stop: 424.

CB993163 AGENCOURT
BM819937 K-EST0088
CB147558 K-EST0203
CB996183 AGENCOURT
BM018750 603646652
BM018834 603646752
BM828076 K-EST0100
BM750435 K-EST0026
BM042219 603616172
BG761095 602717425
BC023582 Homo sapi
BC048808 Homo sapi
BM042052 603616054
BQ678675 AGENCOURT
BQ876328 AGENCOURT
BU179764 AGENCOURT
AY418122 Homo sapi
BU173702 AGENCOURT
BU168445 AGENCOURT
BU174241 AGENCOURT
BI763453 603047463
BG765417 602738887
BU157227 AGENCOURT
BQ680817 AGENCOURT
AY418123 Pan trogl
BM041997 603615880
BU168360 AGENCOURT
BQ836702 AGENCOURT
BU194301 AGENCOURT
BU174317 AGENCOURT
BI862705 603389882
BY084538 BY084538
BY084523 BY084523
BY088484 BY088484
BY088363 BY088363
BY093000 BY093000
BX519821 BX519821
BY708754 BY708754
AK008851 Mus muscu
BQ230697 AGENCOURT
BY084639 BY084639

Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 65 row: C column: 11
High quality sequence stop: 527.
Location/Qualifiers
1. 527
/organism="Homo sapiens"
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/clone="S14K402-65-Cl1"
/cell_line="K402"
/lab_host="Top10P"
/clone_lib="S14K402"
/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
inact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN	Query Match	100.0%	Score 293;	DB 13;	Length 527;
	Best Local Similarity	100.0%;	Pred. No. 3.3e-52;		
	Matches 293;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	GAGGCCCTCTCCACACACAGCCACACAGTCAGCATGAAGCTGTGCTGCTTGCCTCTGTGA	60		
Dd	26	GAGGCCCTCTCCACACACAGCCACACAGTCAGCATGAAGCTGTGCTGCTTGCCTCTGTGA	85		
Qy	61	TGCAGAGCTTGGCCCTCAGCCAGGCACCTGCCCTGCTGCTACTCTCTGCAAAAGCCAGG	120		
Dd	86	TGCAGAGCTTGGCCCTCAGCCAGGCACCTGCCCTGCTGCTACTCTCTGCAAAAGCCAGG	145		
Qy	121	TCAGCAACAGGAGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTCTTGA	180		
Dd	146	TGAGCAACAGGAGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTCTTGA	205		
Qy	191	CCGCGCGATCCGCGAGTTCGCTCCTGACCGCTCATCAGCAAAAGGCTGCAGCTTGA	240		
Dd	206	CCGCGCGATCCGCGAGTTCGCTCCTGACCGCTCATCAGCAAAAGGCTGCAGCTTGA	265		
Qy	241	GGTGGATGACTCAGGAGCTACTACGTGGGCAAGAAATCATCAGTCTGT	293		
Dd	266	GGTGGATGACTCAGGAGCTACTACGTGGGCAAGAAATCATCAGTCTGT	318		

RESULT 4						
CB997275						
LOCUS						
DEFINITION						
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	AGENCOURT_13643348	NIH_MGC_148	Homo sapiens cDNA clone			
	IMAGE:30336859.5,		mRNA sequence.			
ACCESSION	CB997275					
VERSION	CB997275.1	GI:30291795				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					

ORGANISM	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumycota; Eutheria; Primates; Carnivora; Hominidae; Homo.
REFERENCE	1 (bases 1 to 843)
AUTHORS	NIH-MGC http://mgc.nsl.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: Dr. Stefan Hanson cDNA Library Preparation: Michael J. Brownstein (NIHRI) with help and advice from Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM360 row: p column: 20 High quality sequence stop: 612.

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FEATURES
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1. 843
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/mol_type="mRNA"
/db_xref="taxon.9608"
/clone IMAGE:3036859"
/tissue_type="pre-eclamptic placenta"
/lab_host="DHIOB Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: Placenta; Vector: pBluescriptpr; Site_1:
all-XhoI; Site_2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

```

ORIGIN	Query Match	99.5%;	Score	291.4;	DB 14;	Length	843;			
	Best Local Similarity	99.7%;	Pred. No.	8.7e-52;						
	Matches	292;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	GAGGCCCTCTCCACACAGCCACCAGTGACCATGAAGCTGTGCTGCTTGCCCTGTTCGA	60							
Db	52	GAGGCCCTCTCCACACAGCCACCAGTGACCATGAAGCTGTGCTGCTTGCCCTGTTCGA	111							
QY	61	TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGTACTCCTGCAAGGCCAGG	120							
Db	112	TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGTACTCCTGCAAGGCCAGG	171							
QY	121	TGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGCTGA	180							
Db	172	TGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGCTGA	231							
QY	181	CCGCGCGCATCCGCGCAGTTGGCCCTCCCTGACCGGTATATGAGAAAGGCTGCAGCTTGAAC	240							
Db	232	CCGCGCGCATCCGCGCAGTTGGCCCTCCCTGACCGGTATATGAGCAAGGCTGCAGCTTGAAC	291							
QY	241	GGGTGGATGATCTCAGAGACTACTACGTGGGCAAGAGAACATCACGTGCTGT	293							
Db	292	GGGTGGATGACTCAGAGACTACTACGTGGGCAAGAGAACATCACGTGCTGT	344							

RESULT 5	CB993163	851 bp	linear	EST 01-MAY-2003
LOCUS	CB993163			
DEFINITION	AGENCOURT 13628816 NIH MGC 148 Homo sapiens CDNA clone			
	IMAGE:30338013 5', mRNA sequence.			
ACCESSION	CB993163			
VERSION	CB993163.1			
KEYWORDS	GI:30287683			
	EST.			

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: NDAM363 row: p column: 22
 High quality sequence stop: 558.
FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
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 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 148"
 /note="Organ: Placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamHI; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."
ORIGIN
 Query Match 99.5%; Score 291.4; DB 14; Length 851;
 Best Local Similarity 99.7%; Pred. No. 8.7e-52;
 Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GAGGCCCTCTCCACACAGCCACAGTGCACATGAAGGCTGCTGCTGCCCTGTGA 60
 DB 52 GAGGCCCTCTCCACACAGCCACAGTGCACATGAAGGCTGCTGCTGCCCTGTGA 111
 QY 61 TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGTGCTACTCTGCAAGCCGAGG 120
 DB 112 TGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGTGCTACTCTGCAAGCCGAGG 171
 QY 121 TGAGCAACGAGGAGCTGCTGCAGGTGAGAACTCCACCCAGCTGGGGAGCAGTGTGA 180
 DB 172 TGAGCAACGAGGAGCTGCTGCAGGTGAGAACTCCACCCAGCTGGGGAGCAGTGTGA 231
 QY 181 CCGCGCGCATCCGCGCAGTGGCTCTGACCGTCATCAGCAAGGCTGCAGCTGAAT 240
 DB 232 CCGCGCGCATCCGCGCAGTGGCTCTGACCGTCATCAGCAAGGCTGCAGCTGAAT 291
 QY 241 GCCTGGATGACTCAGGACTACTACGTGGGCAAGAGAACATCAGCTGCTGT 293
 DB 292 GCGTGGATGACTCAGGACTACTACGTGGGCAAGAGAACATCAGCTGCTGT 344
RESULT 6
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 LOCUS X-EST0088167 S18N669761 Homo sapiens cDNA clone S18N669761-19-E04
 DEFINITION 5', mRNA sequence.
 ACCESSION BM819937
 VERSION BM819937.1 GI:19176350

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 480)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 19 row: E column: 04
 High quality sequence stop: 480.
FEATURES Location/Qualifiers
 1..480
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 /sex="F"
 /lab_host="Top10P"
 /clone_lib="S18N669761"
 /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
ORIGIN
 Query Match 94.9%; Score 278; DB 12; Length 480;
 Best Local Similarity 100.0%; Pred. No. 4.9e-49;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ACAGCCCAACGATGACCATGAAGGCTGTGCTGCCCTTTGATGTCAGGCTTGCCCC 75
 DB 1 ACAGCCCAACGATGACCATGAAGGCTGTGCTGCCCTTTGATGTCAGGCTTGCCCC 60
 QY 76 TGCAGCCAGGCACTGCCCTGTGCTACTCTCTGCAAGCCAGTGCAGCAACGAGGACT 135
 DB 61 TGCAGCCAGGCACTGCCCTGTGCTACTCTCTGCAAGCCAGTGCAGCAACGAGGACT 120
 QY 136 GCCTCAGGTGAGAACTGCACCCAGTGGGGAGCAGTGTGTCACCGCGCATTCGCG 195
 DB 121 GCCTCAGGTGAGAACTGCACCCAGTGGGGAGCAGTGTGTCACCGCGCATTCGCG 180
 QY 196 CAGTTGGCTCTCTGACCGTCATCAGCAAGGCTCAGCTTGAACCTGCTGATGACTCAC 255
 DB 181 CAGTTGGCTCTCTGACCGTCATCAGCAAGGCTCAGCTTGAACCTGCTGATGACTCAC 240
 QY 256 AGGACTACTACGTGGGCAAGAGAACATCAGCTGCTGT 293
 DB 241 AGGACTACTACGTGGGCAAGAGAACATCAGCTGCTGT 278
RESULT 7

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CB147558
LOCUS       550 bp      mRNA      linear      EST 29-JAN-2003
DEFINITION  K-ESTC203584 L1LSNU354s1 Homo sapiens cDNA clone L1LSNU354s1-29-C07
            5', mRNA sequence.
ACCESSION   CB147558
VERSION     CB147558.1 GI:28129015
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 550)
            Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
COMMENT     Unpublished (2002)
            Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel : +82-42-860-4470
            Fax : +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 29 row: C column: 07
            High quality sequence stop: 550.
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                /sex="M"
                /tissue_type="Liver"
                /cell_type="Polygonal"
                /cell_line="SNU-354"
                /lab_host="Top10P"
                /clone_lib="L1LSNU354s1"
                /note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
                Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tabacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including
                EcoRI site by treatment of T4 RNA ligase and the first
                strand cDNA was synthesized from oligo dT-selected mRNA by
                priming with dT-tailed vector. The dT-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10P, by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library. After analyzing and
                sequencing about 2,000 - 3,000 colonies in original cDNA
                library, the abundant cDNAs were selected and amplified by
                PCR reaction using vector region primer including T7
                promoter as 5' primer and N(dT)14 as 3' primer. The PCR
                products were used as template for synthesis of
                biotinylated single stranded RNA by in vitro transcription
                reaction. The synthesized RNA probes were hybridized with
                antisense single stranded cDNAs prepared from original
                library and incubated with avidin-gel. After removing
                DNA-RNA hybrids by centrifuge, the subtracted cDNA
                libraries were constructed by transformation of the
                remaining DNA into competent cells E. coli Top10P, with
                electroporation method."
ORIGIN
Query Match          94.9%; Score 278; DB 14; Length 550;
Best Local Similarity 100.0%; Pred. No. 5.2e-49;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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ORIGIN

Query Match	94.9%	Score 278;	DB 14;	Length 550;
Best Local Similarity	100.0%;	Pred. No. 5.2e-49;		
Matches 278:	Conservative	0;	Mismatches	0;
	Indels	0;		Gaps

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Db	1	ACAGCCCAACAGTGACATGAAGGCTGTGCTTTCCTGTTGATGCCAGGCTTGGCCC	60
QY	76	TGCAGCAGGCACTGCCCTGCTGCTGTACTCTTCGAAAGCCAGGTGAGCAACGAGGACT	135
Db	61	TGCAGCAGGCACTGCCCTGCTGTGTACTCTTCGAAAGCCAGGTGAGCAACGAGGACT	120
QY	136	GCTTCGAGGTGGAGAAGTGCACCCAGCTGGGGGAGCAGTCTGGACCGCGCGCATCCGCG	195
Db	121	GCTTCGAGGTGGAGAAGTGCACCCAGCTGGGGGAGCAGTCTGGACCGCGCGCATCCGCG	180
QY	196	CAGTTGGCTCTTCGACGCTCATCAGCAAAGGCTGCAGCTTGAATCGCTGGATGACTCAC	255
Db	181	CAGTTGGCTCTTCGACGCTCATCAGCAAAGGCTGCAGCTTGAATCGCTGGATGACTCAC	240
QY	256	AGGACTACTACGTGGGCAAGAAACATCATCGTGTCTGT	293
Db	241	AGGACTACTACGTGGGCAAGAAACATCATCGTGTCTGT	278

RESULT 8
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LOCUS
DEFINITION CB996183 820 bp mRNA linear EST 01-MAY-2003
IMAGE:30337181 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health,
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-re@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM361 row: n column: 06
High quality sequence stop: 597.
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1. 820
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/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site: 1:
all-XhoI; Site 2: BamHI; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTTN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH MGC
Library."

FEATURES
source

ORIGIN

Query Match	94.9%	Score 278	DB 14	Length 550
Best Local Similarity	100.0%	Pred. NO. 5.2e-49		
Matches 278:	Conservative	0: Mismatches	0: Indels	0: Gaps

QY 16 ACAGCCACAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 75
 Db 28 ACAGCCACAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 87
 QY 76 TGCAGCAGGCACTGCTGCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACAGGACT 135
 Db 88 TGCAGCAGGCACTGCTGCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACAGGACT 147
 QY 136 GCGTGCAGTGTGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGCG 195
 Db 148 GCGTGCAGTGTGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGCG 207
 QY 196 CAGTTGGCTCTGACCGCTCATCAGCAAGGCTGCAGCTTGAATGCGTGGATGACTCAC 255
 Db 208 CAGTTGGCTCTGACCGCTCATCAGCAAGGCTGCAGCTTGAATGCGTGGATGACTCAC 267
 QY 256 AGGACTACTAGCTGGGCAAGAGACATCAGTGTGT 293
 Db 268 AGGACTACTAGCTGGGCAAGAGACATCAGTGTGT 305

RESULT 9
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 LOCUS 60364652F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5428261 5',
 DEFINITION mRNA sequence.
 ACCESSION BM018750
 VERSION BM018750.1 GI:16533104
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 827)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1895 row: 9 column: 14
 High quality sequence stop: 810.
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 /db_xref="taxon:9606"
 /clone="IMAGE:5428261"
 /tissue_type="astrocytoma grade IV, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_98"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

FEATURES
 source
 Query Match 93.9%; Score 275; DB 12; Length 827;
 Best Local Similarity 100.0%; Pred. No. 2.6e-48;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 GCCCACCAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 78

ORIGIN

Query Match 93.9%; Score 275; DB 12; Length 827;
 Best Local Similarity 100.0%; Pred. No. 2.6e-48;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 GCCCACCAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 78

Db 2 GCCCACCAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 61
 QY 79 AGCAGGCACTGCTGCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACAGGACTGCC 138
 Db 62 AGCAGGCACTGCTGCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACAGGACTGCC 121
 QY 139 TGCAGTGTGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGCGCAG 198
 Db 122 TGCAGTGTGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCATCCGCGCAG 181
 QY 199 TTGGCTCTGACCGCTCATCAGCAAGGCTGCAGCTTGAATGCGTGGATGACTCACAGG 258
 Db 182 TTGGCTCTGACCGCTCATCAGCAAGGCTGCAGCTTGAATGCGTGGATGACTCACAGG 241
 QY 259 ACTACTACGCTGGGCAAGAGACATCAGTGTGT 293
 Db 242 ACTACTACGCTGGGCAAGAGACATCAGTGTGT 276

RESULT 10
 BM018834
 LOCUS 603646752F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5428285 5',
 DEFINITION mRNA sequence.
 ACCESSION BM018834
 VERSION BM018834.1 GI:16533188
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 972)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1895 row: h column: 14
 High quality sequence stop: 831.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5428285"
 /tissue_type="astrocytoma grade IV, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_98"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

FEATURES
 source
 Query Match 93.9%; Score 275; DB 12; Length 972;
 Best Local Similarity 100.0%; Pred. No. 2.6e-48;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 GCCCACCAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 78
 Db 2 GCCCACCAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 61

ORIGIN

Query Match 93.9%; Score 275; DB 12; Length 972;
 Best Local Similarity 100.0%; Pred. No. 2.6e-48;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 GCCCACCAGTACCATGAAGGCTGTGCTTGGCTTGTGATGCGAGGCTTGGCCC 78

QY 79 AGCCAGGCACTGCCTGTGCTACTCTCCAAAGCCAGGTGAGCAACGAGGACTGCC 138
 Db 62 AGCCAGGCACTGCCTGTGCTACTCTCCAAAGCCAGGTGAGCAACGAGGACTGCC 121
 QY 139 TGCAGGTGGAGAACTGACCCAGTGGGAGCAGTCTGGACCGCGCATCCGGCAG 198
 Db 122 TGCAGGTGGAGAACTGACCCAGTGGGAGCAGTCTGGACCGCGCATCCGGCAG 181
 QY 199 TTGGCTCTCCTGACCGTATCAGCAAAAGCTGCAGCTTGAACCTGGTGGATGACTCACAGG 258
 Db 182 TTGGCTCTCCTGACCGTATCAGCAAAAGCTGCAGCTTGAACCTGGTGGATGACTCACAGG 241
 QY 259 ACTACTAGTGGGCAAGAAACATCAGTCTGT 293
 Db 242 ACTACTAGTGGGCAAGAAACATCAGTCTGT 276

RESULT 11
 BM828076 547 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0100821 S9SNU601 Homo sapiens cDNA clone S9SNU601-48-D10 5',
 DEFINITION mRNA sequence.

ACCESSION BM828076
 VERSION BM828076.1 GI:19184485

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 547)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 48 row: D column: 10
 High quality sequence stop: 547.

FEATURES Location/Qualifiers
 1..547

source
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 /db_xref="taxon:9606"
 /clone="S9SNU601-48-D10"
 /sex="M"
 /tissue_type="Ascites"
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 /lab_host="Top10F"
 /clone_lib="S9SNU601"
 /note="Organ: Stomach; Vector: pME18-FL3; Site:1: XhoI;
 Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including SfiI
 site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized with Superscript II using SfiI
 oligo-dT primer. After first strand synthesis, RNA was
 degraded by NaOH treatment and cDNA was amplified by PCR
 reaction. The PCR products were digested with SfiI and
 cloned into BsalI-digested pME18-FL3 vector. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 93.7%; Score 274.4; DB 12; Length 547;
 Best Local Similarity 99.6%; Pred. No. 3e-48; Mismatches 0; Gaps 0;
 Matches 275; Conservative 0; Indels 1; Gaps 0;
 QY 18 AGCCACCACTGACCATGAGGCTGTGCTGTTCCTTGTGATGGCAGGCTTGGCCCTG 77
 Db 1 AGCCACCACTGACCATGAGGCTGTGCTGTTCCTTGTGATGGCAGGCTTGGCCCTG 60
 QY 78 CAGCCAGGCACTGCCTGTGCTGTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 137
 Db 61 CAGCCAGGCACTGCCTGTGCTGTCTCTCAAGCCAGGTGAGCAACGAGGACTGC 120
 QY 138 CTGCAGGTGGAGAACTGACCCAGTGGGGAGCAGTGTGACCGCGCATCCGGCAG 197
 Db 121 CTGCAGGTGGAGAACTGACCCAGTGGGGAGCAGTGTGACCGCGCATCCGGCAG 180
 QY 198 GTTGGCTCTCCTGACCGTATCAGCAAAAGCTGCAGCTTGAACCTGGTGGATGACTCACAG 257
 Db 181 GTTGGCTCTCCTGACCGTATCAGCAAAAGCTGCAGCTTGAACCTGGTGGATGACTCACAG 240
 QY 258 GACTACTAGTGGGCAAGAAACATCAGTCTGT 293
 Db 241 GACTACTAGTGGGCAAGAAACATCAGTCTGT 276

RESULT 12

BM750435

LOCUS K-EST0026004 S9SNU601 Homo sapiens cDNA clone S9SNU601-30-E01 5',
 DEFINITION mRNA sequence.

ACCESSION BM750435

VERSION BM750435.1 GI:19080053

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 315)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 30 row: E column: 01
 High quality sequence stop: 315.

FEATURES Location/Qualifiers
 1..315

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S9SNU601-30-E01"
 /sex="M"
 /tissue_type="Ascites"
 /cell_type="Epithelial"
 /cell_line="SNU-601"
 /lab_host="Top10F"
 /clone_lib="S9SNU601"
 /note="Organ: Stomach; Vector: pME18-FL3; Site:1: XhoI;
 Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including SfiI
 site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized with Superscript II using SfiI
 oligo-dT primer. After first strand synthesis, RNA was
 degraded by NaOH treatment and cDNA was amplified by PCR
 reaction. The PCR products were digested with SfiI and
 cloned into BsalI-digested pME18-FL3 vector. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:35:58 ; Search time 1397.08 Seconds
(without alignments)
8655.682 Million cell updates/sec

Title: US-09-079-874-3

Perfect score: 279
Sequence: 1 CAGTGACATGAGGCTGTG.....CACGTGCTGTGACACCGACT 279

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb.htg.*
3: gb.in.*
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5: gb.ov.*
6: gb.pat.*
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9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
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40: em.htgo.mus.*
41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	279	100.0	946	9	HSA297436	AJ297436 Homo sapi
2	279	100.0	990	6	AX014204	AX014204 Sequence
3	279	100.0	990	6	BD205072	BD205072 Human nuc
4	279	100.0	990	9	AF043498	AF043498 Homo sapi
5	279	100.0	998	6	AR162849	AR162849 Sequence
6	279	100.0	998	6	AR302232	AR302232 Sequence
7	279	100.0	998	6	AX080304	AX080304 Sequence
8	279	100.0	998	6	BD193367	BD193367 Prostate
9	277.4	99.4	979	6	BD076397	BD076397 Human pro
10	277	99.3	288	6	AR026990	AR026990 Sequence
11	277	99.3	494	6	AR026974	AR026974 Sequence
12	277	99.3	1015	9	BC023582	BC023582 Homo sapi
13	275.8	98.9	998	6	BD264314	BD264314 PSCA: pro
14	271	97.1	372	6	AX155553	AX155553 Sequence
15	269.8	96.7	373	6	AX884747	AX884747 Sequence
16	269.8	96.7	373	6	BD024357	BD024357 Sequence
17	269.4	96.6	369	6	BD076387	BD076387 Human pro
18	268.8	96.3	373	6	BD076369	BD076369 5' EST of
19	260	93.2	960	6	AR410610	AR410610 Sequence
20	260	93.2	960	6	AX201328	AX201328 Sequence
21	260	93.2	960	6	AX597426	AX597426 Sequence
22	260	93.2	960	6	BD075381	BD075381 Secretory
23	260	93.2	960	6	BD172241	BD172241 Secreted
24	260	93.2	960	6	BD172560	BD172560 Secreted
25	260	93.2	960	6	BD172879	BD172879 Secreted
26	260	93.2	960	6	BD173198	BD173198 Secreted
27	260	93.2	960	6	BD175232	BD175232 Secretory
28	260	93.2	960	9	AX155892	AX155892 Homo sapi
29	251.8	90.3	372	6	AX155567	AX155567 Sequence
30	250.2	89.7	372	6	AR026988	AR026988 Sequence
31	227	81.4	286	6	AR026992	AR026992 Sequence
32	218.4	78.3	232	6	AR026992	AR026992 Sequence
33	152.4	54.6	864	10	AF319173	AF319173 Mus muscu
34	148.4	53.2	441	6	AR162850	AR162850 Sequence
35	148.4	53.2	441	6	BD264315	BD264315 PSCA: pro
36	148.4	53.2	441	6	AR302233	AR302233 Sequence
37	148.4	53.2	441	6	AX080306	AX080306 Sequence
38	148.4	53.2	441	6	BD193368	BD193368 Prostate
39	112.4	40.3	2532	6	AX747544	AX747544 Sequence
40	112.4	40.3	2532	9	AK092432	AK092432 Homo sapi
41	112.4	40.3	100079	9	AC108002	AC108002 Homo sapi
42	112.4	40.3	103247	2	AF176678	AF176678 Homo sapi
43	112.4	40.3	105156	2	AF235094	AF235094 Homo sapi
44	112.4	40.3	157839	2	AC015718	AC015718 Homo sapi
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ALIGNMENTS

RESULT 1
HSA297436
LOCUS HSA297436 946 bp mRNA linear PRI 13-OCT-2000
DEFINITION Homo sapiens mRNA for prostate stem cell antigen (PSCA gene).
ACCESSION AJ297436
VERSION AJ297436.1 GI:9367211
KEYWORDS prostate stem cell antigen; PSCA gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bahrenberg,G., Brauers,A., Joost,H.G. and Jakse,G.
TITLE Reduced expression of PSCA, a member of the Ly-6 family of cell surface antigens, in bladder, esophagus, and stomach tumors

Pred. No. is the number of results predicted by chance to have a

JOURNAL Biochem. Biophys. Res. Commun. 275 (3), 783-788 (2000)
 MEDLINE 204311743
 PUBMED 10973799
 REFERENCE 2 (bases 1 to 946)
 AUTHORS Bahrenberg, G.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUL-2000) Bahrenberg G., Institut fuer Pharmakologie und Toxikologie, RWTH Aachen, Wendingweg2, Aachen, NRW, 52057, GERMANY

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 /country="Germany"
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 CDS 20..391
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 /db_xref="COA:043653"
 /db_xref="SWISS-PROT:O43653"
 /translation="MKAVLLALIMAGLQFPTALLCYSCQVSNEDCLQVENCQL
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 9.6e-48;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGCTGTGCTTGCCTGTGTGATGGGAGGCTTGGCCCTGCAGCCAG 60
 DB 12 CAGTGACCATGAAGCTGTGCTTGCCTGTGTGATGGGAGGCTTGGCCCTGCAGCCAG 71
 QY 61 GCATGCCCCCTGCTGTGCTACTCTTCGAAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 120
 DB 72 GCATGCCCCCTGCTGTGCTACTCTTCGAAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 131
 QY 121 TGGAGAACTGCACCTGAGGAGGAGTGTGCTGAACTGGATGATCTCAGGACTACT 180
 DB 132 TGGAGAACTGCACCTGAGGAGGAGTGTGCTGAACTGGATGATCTCAGGACTACT 191
 QY 181 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAATCGGTGGATGACTCAGGACTACT 240
 DB 192 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAATCGGTGGATGACTCAGGACTACT 251
 QY 241 ACGTGGGCAAGAGAACATCAGCTGCTGTGATGATCTCAGGACTACT 279
 DB 252 ACGTGGGCAAGAGAACATCAGCTGCTGTGATGATCTCAGGACTACT 290

RESULT 2
 AX014204
 LOCUS AX014204 990 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 108 from Patent WO9954447.
 ACCESSION AX014204
 VERSION AX014204.1 GI:10040611
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and Pilarsky, C.
 TITLE Human nucleic acid sequences of bladder tumour tissue
 JOURNAL Patent: WO 9954447-A 108 28-OCT-1999;
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)

FEATURES
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 100.0%; Score 279; DB 6; Length 990;
 Best Local Similarity 100.0%; Pred. No. 9.6e-48;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGCTGTGCTTGCCTGTGTGATGGGAGGCTTGGCCCTGCAGCCAG 60
 DB 10 CAGTGACCATGAAGCTGTGCTTGCCTGTGTGATGGGAGGCTTGGCCCTGCAGCCAG 69
 QY 61 GCATGCCCCCTGCTGTGCTACTCTTCGAAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 120
 DB 70 GCATGCCCCCTGCTGTGCTACTCTTCGAAAGCCCAAGGTGAGCAACGAGGACTGGCTGCAGG 129
 QY 121 TGGAGAACTGCACCTGAGGAGGAGTGTGCTGAACTGGATGATCTCAGGACTACT 180
 DB 130 TGGAGAACTGCACCTGAGGAGGAGTGTGCTGAACTGGATGATCTCAGGACTACT 189
 QY 181 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAATCGGTGGATGACTCAGGACTACT 240
 DB 190 TCCTGACCGTATCAGCAAGGCTGCAGCTTGAATCGGTGGATGACTCAGGACTACT 249
 QY 241 ACGTGGGCAAGAGAACATCAGCTGCTGTGATGATCTCAGGACTACT 279
 DB 250 ACGTGGGCAAGAGAACATCAGCTGCTGTGATGATCTCAGGACTACT 288

RESULT 3
 BD205072 990 bp DNA linear PAT 17-JUL-2003
 LOCUS Human nucleic acid sequence originating in cystic cancer tissue.
 DEFINITION
 ACCESSION BD205072.1 GI:33014842
 VERSION JP 2002512023-A/26.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 990)
 AUTHORS Specht, T., Hinzmann, B., Schmitt, A., Pilarsky, C., Dahl, E. and Rosenthal, A.
 TITLE Human nucleic acid sequence originating in cystic cancer tissue
 JOURNAL Patent: JP 2002512023-A 26 23-APR-2002;
 METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH

COMMENT
 OS Homo sapiens (human)
 PN JP 2002512023-A/26
 PD 23-APR-2002
 PF 15-APR-1999 JP 2000544779
 PR 21-APR-1998 DE 198 18 619.3
 PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY, PI EDGAR DAHL,
 PI ANDRE ROSENTHAL
 PC C12N15/02, A61K39/395, A61K38/00, A61K48/00, A61P13/10,
 PC A61P35/00,
 PC C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12P21/08, C12Q1/68, PC C12N15/00,
 PC A61K37/02, C12N5/00
 CC Human nucleic acid sequence originating in cystic cancer CC

PH Key tissue Location/Qualifiers
 FT source 1..990

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Dd	70	GCACTGCCCTGCTGTGTACTCTCTGAAGCCAGGTGACNCGAGGACTGCCTGCAGG	129
QY	121	TGGAGAATGCACCCAGCTCGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCC	180
Dd	130	TGGAGAATGCACCAGCTCGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCC	189
QY	181	TCCTGCGGTTCATCAGCAAAAGGCTGCAGCTTGAATCGCTGGATGACTCACAGGACTACT	240
Dd	190	TCCTGACCGTTCATCAGCAAAAGGCTGCAGCTTGAATCGCTGGATGACTCACAGGACTACT	249
QY	241	ACGTGGCGAAGAAGAACATCACGTGCTGTGACCCGACT	279

250 ACGTGGGCAAGAAACATCACTGCTGTGACACCGACT 288

RESULT 6
 AR302232 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REITER
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 AR302232
 Sequence 1 from patent US 6541212.
 AR302232
 AR302232.1 GI:31690451
 Unknown.
 Unknown.
 Unclassified.
 1 (bases 1 to 998)
 Reiter,R.E. and Witte,O.N.
 Methods for detecting prostate stem cell antigen protein
 Patent: US 6541212-A 1 01-APR-2003;
 Location/Qualifiers
 1..998
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN

Query Match	100.0%	Score 279;	DB 6;	Length 998;
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DB	10	CAGTGACCATGAAGCGTGTGCTTCCCTGTGTGATGTCAGCGCTTGGCCCTGCAAGCCAG	69	
QY	61	GCATGCCCTGCTGTGCTACTCTCGAAAGCCAGGTGAGCAACGAGNCTGCTCTGCAGG	120	
DB	70	GCATCGCCCTGCTGTGCTACTCTCGAAAGCCAGGTGAGCAACGAGGACTGCTCTGCAGG	129	
QY	121	TGGAGAACTGGACCCAGCTGGGGGAGCAGTGTCTGGACCGCGCGGCATCCGCGCAGTGTGCC	180	
DB	130	TGGAGAACTGGACCCAGCTGGGGGAGCAGTGTCTGGACCGCGCGGCATCCGCGCAGTGTGCC	189	
QY	181	TCTTGACCGTCAATCAGCAAAAGCTTGACCTTGAACTGCGTGGATGACTACAGGACTACT	240	
DB	190	TCTTGACCGTCAATCAGCAAAAGCTTGACCTTGAACTGCGTGGATGACTACAGGACTACT	249	
QY	241	ACGTGGGCAAGAAGAACATCACTGCTGTGCACCCGACT	279	
DB	250	ACGTGGGCAAGAAGAACATCACTGCTGTGCACCCGACT	288	

RESULT 7

AX080304	AX080304	998 bp	DNA	linear	PAT 22-FEB-2001
LOCUS	Sequence 1 from Patent WO0105427.				
DEFINITION	AX080304				
ACCESSION	AX080304				
VERSION	AX080304.1	GI:13159773			

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Best Local Similarity	100.0%;	Pred. NO.	9.6e-48;				
Matches	279;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0						

Qy	1	CAGTGCACATCAAGGCTGTGCTGCTTCCCTGTGTGATGTCAGGCTTTGGCCCTGCAGCCAG	60
Db	10	CAGTGCACCATGAAGCTGTGCTGCTTCCCTGTGTGATGTCAGGCTTTGGCCCTGCAGCCAG	69
Qy	61	GCACCTGCCCTGCTGTACTCTTGCAAGCCGAGGTGACACGAGGACTGCCTGCAG	120
Db	70	GCACCTGCCCTGCTGTACTCTTGCAAGCCGAGGTGACACGAGGACTGCCTGCAG	129
Qy	121	TGGAGAACTGCACCCAGCTGGGGGAGCAGTGCTGGAACCGCGGCATCCGGCGAGTTGGCC	180
Db	130	TGGAGAACTGCACCCAGCTGGGGGAGCAGTGCTGGAACCGCGGCATCCGGCGAGTTGGCC	189
Qy	181	TCTGCACCGTATCAGCAAGGCTGCAGCTTGACCTGCGTGGATGACTCACAGGACTACT	240
Db	190	TCTGCACCGTATCAGCAAGGCTGCAGCTTGAACTGCTGGATGACTCACAGGACTACT	249
Qy	241	ACGTGGGCAAGAAGACATCATCGTCTGTGACCCGACT	279
Db	250	ACGTGGGCAAGAAGACATCATCGTGTGTGACCCGACT	288

RESULT 8	998 bp	DNA	linear	PAT 17-JUL-2000
BD193367				
LOCUS				
DEFINITION	Prostate stem cell antigen.			
ACCESSION	BD193367			
VERSION	BD193367.1 GI:33003106			
KEYWORDS	JP 2002511740-A/1.			
SOURCE	unidentified			
ORGANISM	unidentified			
REFERENCE	unclassified.			
AUTHORS	1 (bases 1 to 998)			
TITLE	Reiter,R. and Witte,O.			
JOURNAL	Prostate stem cell antigen			
COMMENT	Patent: JP 2002511740-A 1 16-APR-2002; THE REGENTS OF THE UNIVERSITY OF CALIFORNIA OS Unidentified PN JP 2002511740-A/1 PD 16-APR-2002 PP 10-MAR-1998 JP 1998539713 PP 10-MAR-1997 US 08/814279, 12-JAN-1998 US 60/071141 PR			

	Query Match	100.0%	Score 279;	DB 6;	Length 999;
	Best Local Similarity	100.0%;	Pred.No.9.6e-48;		
	Matches 279;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0
Qy	1	CAGTGACCATGAAGCCTGCTGCTGTCCCTGTGTGATGGCAGGCTTGGCCCTGCACCCAG	60		
Db	10	CAGTGACCATGAAGCCTGCTGCTGTCCCTGTGTGATGGCAGGCTTGGCCCTGCACCCAG	69		
Qy	61	GCAC'TGCCCTGCTGTGCTACTCTCTGAAAGCCAGGCTGAGCAACAGAGGACTGCCTCGAG	120		
Db	70	GCAC'TGCCCTGCTGTGCTACTCTCTGAAAGCCAGGCTGAGCAACAGAGGACTGCCTCGAG	129		


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QY 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 180
Db 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 189
QY 181 TCTGACCTCATCAGCAAGGCTGCAGCTTGAATGGCTGGATGACTCAGAGGACTACT 240
Db 190 TCTGACCTCATCAGCAAGGCTGCAGCTTGAATGGCTGGATGACTCAGAGGACTACT 249
QY 241 ACGTGGGCAAGAGAACATCAGTGTGTGACACCGACT 279
Db 250 ACGTGGGCAAGAGAACATCAGTGTGTGACACCGACT 288

RESULT 9
BD076397 979 bp DNA linear PAT 27-AUG-2002
LOCUS Human protein having transmembrane domain and DNA encoding the
DEFINITION same.
ACCESSION BD076397
VERSION BD076397.1 GI:22622000
KEYWORDS JP 2001519154-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 979)
AUTHORS Kato,S., Kimura,T., Sekine,S. and Kobayashi,M.
TITLE Human protein having transmembrane domain and DNA encoding the same
JOURNAL Patent: JP 2001519154-A 11 23-OCT-2001;
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
COMMENT OS Homo sapiens (human)
PN JP 2001519154-A/11
PD 23-OCT-2001
PF 05-OCT-1998 JP 2000515001
PI SEISHI KATO,TOMOKO KIMURA,SHINGO SEKINE,MIDORI KOBAYASHI PC
C12N15/09,C07K14/47,C12N5/10,C12N15/00,C12N5/00 CC Human protein
having transmembrane domain
and DNA encoding the
CC same
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Best Local Similarity 99.6%; Pred. No. 2.1e-47;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTGTGCTTGCCTGTGATGGCAGGCTTGGCCCTGCAGCCAG 60
Db 8 CAGTGACCATGAAGGCTGTGCTGTGCTTGCCTGTGATGGCAGGCTTGGCCCTGCAGCCAG 67
QY 61 GCACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGG 120
Db 68 GCACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGG 127
QY 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 180
Db 128 TGAAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 187
QY 181 TCTGACCTCATCAGCAAGGCTGCAGCTTGAATGGCTGGATGACTCAGAGGACTACT 240
Db 188 TCTGACCTCATCAGCAAGGCTGCAGCTTGAATGGCTGGATGACTCAGAGGACTACT 247
QY 241 ACGTGGGCAAGAGAACATCAGTGTGTGACACCGACT 279
Db 248 ACGTGGGCAAGAGAACATCAGTGTGTGACACCGACT 286
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RESULT 10
AR026990 288 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 23 from patent US 5856136.
DEFINITION AR026990
ACCESSION AR026990
VERSION AR026990.1 GI:5937830
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 288)
AUTHORS Au-Young,J.
TITLE Human stem cell antigens
JOURNAL Patent: US 5856136-A 23 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..288
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 62
Db 1 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
QY 63 ACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGGTG 122
Db 61 ACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGGTG 120
QY 123 GAGAACTGCAACGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCCTC 182
Db 121 GAGAACTGCAACGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCCTC 180
QY 183 CTGACCTCATCAGCAAGGCTGCAGCTTGAATGGCTGGATGACTCAGAGGACTACTAC 242
Db 181 CTGACCTCATCAGCAAGGCTGCAGCTTGAATGGCTGGATGACTCAGAGGACTACTAC 240
QY 243 GTGGGCAAGAGAACATCAGCTGTGTGACCCGACT 279
Db 241 GTGGGCAAGAGAACATCAGCTGTGTGACCCGACT 277

RESULT 11
AR026974 494 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 4 from patent US 5856136.
DEFINITION AR026974
ACCESSION AR026974
VERSION AR026974.1 GI:5937814
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 494)
AUTHORS Au-Young,J.
TITLE Human stem cell antigens
JOURNAL Patent: US 5856136-A 4 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..494
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 99.3%; Score 277; DB 6; Length 494;
Best Local Similarity 100.0%; Pred. No. 2.7e-47;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 62
Db 1 GTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:33:41 ; Search time 182.385 Seconds
(without alignments)
6498.587 Million cell updates/sec

Title: US-09-079-874-3

Perfect score: 279

Sequence: 1 CAGTGACCATGAAGCTGTG.....CACGTGCTGTGACACCGACT 279

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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1: Geneseq1980s: *
2: Geneseq1990s: *
3: Geneseq2000s: *
4: Geneseq2001as: *
5: Geneseq2001bs: *
6: Geneseq2002s: *
7: Geneseq2003as: *
8: Geneseq2003bs: *
9: Geneseq2003cs: *
10: Geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	279	100.0	279	2	AAV80388 Nucleotid
2	279	100.0	279	2	AAV68605 Human PSI
3	279	100.0	990	7	ACC51040 Human bla
4	279	100.0	990	7	ABQ83853 Human PSC
5	279	100.0	990	9	ADCO9589 PSCA cDNA
6	279	100.0	998	4	ABK09980 Human pro
7	279	100.0	998	5	AAZ27971 Human pro
8	279	100.0	1023	2	AAV80397 Consensus
9	279	100.0	1023	2	AAV68613 Human PSI
10	279	100.0	1023	2	AAV68614 Human PSI
11	279	100.0	1028	9	ADBS3926 Human pro
12	277.4	99.4	979	2	AAV36801 Human tra
13	277.4	99.4	998	2	AAV33691 Human pro
14	277.4	99.4	998	3	AAA48374 Human ste
15	277	99.3	288	2	AAV38061 Human ste
16	277	99.3	494	2	AAV38045 Human ste
17	277	99.3	372	2	AAV80396 Nucleotid
18	271	97.1	372	4	AAO08171 Human pro
19	269.8	96.7	373	3	AAO0612 Human tra
20	269.4	96.6	369	2	AAV36800 Human tra
21	269	96.4	293	2	AAV80387 Nucleotid
22	269	96.4	293	2	AAV68604 Human PSI
23	268.8	96.3	373	2	AAV40622 Human sec

24	260	93.2	960	2	AAV52217 Protein P
25	260	93.2	960	3	AdC78337 Human PRO
26	260	93.2	960	4	Asf72375 Human PRO
27	260	93.2	960	6	ABK4257 CDNA enco
28	260	93.2	960	7	ACA59909 Human PRO
29	260	93.2	960	7	ACA58306 CDNA enco
30	260	93.2	960	7	ACA60013 Human CDN
31	260	93.2	960	7	AdC07413 Novel hum
32	260	93.2	960	7	ABX71461 Human CDN
33	260	93.2	960	7	ACH06793 Human sec
34	260	93.2	960	7	ABX96030 Human sec
35	260	93.2	960	7	ACA03351 CDNA enco
36	260	93.2	960	7	AdC20018 Human sec
37	260	93.2	960	7	ACA54821 Novel hum
38	260	93.2	960	8	AdC19656 Human sec
39	260	93.2	960	8	ADB29222 Human sec
40	260	93.2	960	8	ADA18078 Human sec
41	260	93.2	960	8	ACD66803 Human CDN
42	260	93.2	960	8	ACD82964 Human PRO
43	260	93.2	960	8	ADA16053 Human sec
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ALIGNMENTS

RESULT 1

AAV80388

ID AAV80388 standard; DNA; 279 BP.

XX

AC AAV80388;

XX

DT 23-FEB-1999 (first entry)

XX

DE Nucleotide sequence of UT116 gene-specific clone 1891065.

XX

KW UT116; urinary tract; epitope; antigen; detection; diagnosing;

KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;

KW metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO9851824-Al.

XX

PD 19-NOV-1998.

XX

PF 15-MAY-1998; 98WO-US009972.

XX

PR 15-MAY-1997; 97US-00856652.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;

PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;

PI Stroupe SD;

XX

DR WPI; 1999-045237/04.

XX

PT New method for detecting diseases of the urinary tract - comprises use of

PT a UT116 polynucleotide, protein or antibodies, used for preventing and

PT treating urinary tract infections and cancer.

XX

PS Claim 1; Fig 1A-C; 113pp; English.

XX

CC Sequences AAV80396 to AAV80398 represent partially overlapping nucleotide

CC sequences of the UT116 gene-specific clones derived from urinary tract

CC tissue. The invention relates to a method of detecting the presence of a

CC target UT116 polynucleotide in a test sample using these UT116-specific

CC sequences. Host cells transfected with an expression vector containing

CC the UT116 gene can be used to produce a UT116 polypeptide recombinantly.

CC This polypeptide has at least one UT116 epitope which can be used in a

CC method for detecting UT116 antigen in a test sample. The polynucleotides

CC and polypeptides are useful for detecting, diagnosing, monitoring,
 CC staging, prognosticating, in vivo imaging, preventing, treating or
 CC determining the predisposition of a subject to diseases and conditions of
 CC the urinary tract, such as urinary tract cancer. Antibodies specifically
 CC binding to an epitope of Uril6 antigen, and agonists are useful for
 CC treating urinary tract diseases, tumors and metastases

XX
 SQ Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 279; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.3e-59;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGAGCCAG 60

Db 1 CAGTGACCATGAAGGCTGTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGAGCCAG 60

QY 61 GCATGCGCTCTGTGCTACTCTTGCAGAGCCAGGTGAGCAAGGAGTGGCTGAGG 120

Db 61 GCATGCGCTCTGTGCTACTCTTGCAGAGCCAGGTGAGCAAGGAGTGGCTGAGG 120

QY 121 TGGAGAACTGACCCAGTGGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 180

Db 121 TGGAGAACTGACCCAGTGGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 180

QY 181 TCCTGACCGTATCAGCAAGGCTGAGCTTGAAGTGGATGACTACAGGACTACT 240

Db 181 TCCTGACCGTATCAGCAAGGCTGAGCTTGAAGTGGATGACTACAGGACTACT 240

QY 241 ACGTGGGCAAGAAGCAATCAGTGGCTGTGACACCGGACT 279

Db 241 ACGTGGGCAAGAAGCAATCAGTGGCTGTGACACCGGACT 279

RESULT 2

AAV68605
 ID AAV68605 standard; cDNA; 279 BP.

XX
 AC AAV68605;

DT 16-MAR-1999 (first entry)

DE Human PS116 EST clone 1891065.

KW Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 KW detection; therapy; prostate cancer; metastasis; ss.

OS Homo sapiens.

PN WO9851805-A1.

PD 19-NOV-1998.

XX 15-MAY-1998; 98WO-US010041.

XX 15-MAY-1997; 97US-00856653.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD;

XX WPI; 1999-045234/04.

XX New method for detecting diseases of the prostate - comprises use of a
 PT PS116 polynucleotide, protein or antibodies, useful for preventing and
 PT treating prostate infections and cancer.

XX Claim 1; Page 92; 118pp; English.

XX This sequence represents an expressed sequence tag (EST) clone of the
 CC PS116 gene isolated from a human prostate tissue library. This sequence

CC can be used in the method of the invention for detecting a target PS116
 CC polynucleotide (PN), that comprises: contacting a sample with at least 1
 CC PS116-specific PN or complement; and detecting the target PS116 PN, where
 CC the specific PN has at least 50% identity with this sequence. The PNs,
 CC PS116 polypeptides or PS116 amplicons are used to detect prostate
 CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
 CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
 CC solid phase. The polypeptides are used for detecting PS116-specific Abs
 CC in a sample, and for producing Abs after immunising a subject. Plasmids
 CC encoding PS116 epitopes can also be administered to a subject to obtain
 CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
 CC staging, monitoring, prognosticating, in vivo imaging, preventing,
 CC treating or determining the predisposition of a subject to diseases and
 CC conditions of the prostate, such as prostate cancer. The Abs and agonists
 CC or inhibitors are useful for treating prostate diseases, tumours and
 CC metastases

XX
 SQ Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 279; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.3e-59;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGAGCCAG 60

Db 1 CAGTGACCATGAAGGCTGTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGAGCCAG 60

QY 61 GCATGCGCTCTGTGCTACTCTTGCAGAGCCAGGTGAGCAAGGAGTGGCTGAGG 120

Db 61 GCATGCGCTCTGTGCTACTCTTGCAGAGCCAGGTGAGCAAGGAGTGGCTGAGG 120

QY 121 TGGAGAACTGACCCAGTGGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 180

Db 121 TGGAGAACTGACCCAGTGGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 180

QY 181 TCCTGACCGTATCAGCAAGGCTGAGCTTGAAGTGGATGACTACAGGACTACT 240

Db 181 TCCTGACCGTATCAGCAAGGCTGAGCTTGAAGTGGATGACTACAGGACTACT 240

QY 241 ACGTGGGCAAGAAGCAATCAGTGGCTGTGACACCGGACT 279

Db 241 ACGTGGGCAAGAAGCAATCAGTGGCTGTGACACCGGACT 279

RESULT 3

ACC51040
 ID ACC51040 standard; cDNA; 990 BP.

XX
 AC ACC51040;

DT 12-JUN-2003 (first entry)

XX Human bladder cancer associated cDNA sequence SEQ ID NO:168.

DE Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.

KW Homo sapiens.

OS Homo sapiens.

PN WO2003003906-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021338.

XX 03-JUL-2001; 2001US-0302814P.

XX 03-AUG-2001; 2001US-0310099P.

XX 08-NOV-2001; 2001US-0343705P.

XX 13-NOV-2001; 2001US-0350666P.

XX 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Aziz N;

CC invention relates to a method of detecting the presence of a target Utl16
 CC polynucleotide in a test sample using Utl16-specific sequences (AAV80386
 CC to AAV80397). Host cells transfected with an expression vector containing
 CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
 CC This polypeptide has at least one Utl16 epitope which can be used in a
 CC method for detecting Utl16 antigen in a test sample. The polynucleotides
 CC and polypeptides are useful for detecting, diagnosing, monitoring,
 CC staging, prognosticating, in vivo imaging, preventing, treating or
 CC determining the predisposition of a subject to diseases and conditions of
 CC the urinary tract, such as urinary tract cancer. Antibodies specifically
 CC binding to an epitope of Utl16 antigen, and agonists are useful for
 CC treating urinary tract diseases, tumours and metastases
 XX
 SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;
 Query Match 100.0%; Score 279; DB 2; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 1.7e-59;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGCCTGCAGCCAG 60
 DB 50 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGCCTGCAGCCAG 109
 QY 61 GCATGCCCCCTGTGCTTACTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 120
 DB 110 GCATGCCCCCTGTGCTTACTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 169
 QY 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 180
 DB 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 229
 QY 181 TCCTGACCGTTCATCAGCAAGAGCTGCACTTGAACCTGGTGATCACTCAGGACTACT 240
 DB 230 TCCTGACCGTTCATCAGCAAGAGCTGCACTTGAACCTGGTGATCACTCAGGACTACT 289
 QY 241 ACGTGGGCAAGAAGACATCAGCTGCTGTGACACCGACT 279
 DB 290 ACGTGGGCAAGAAGACATCAGCTGCTGTGACACCGACT 328

RESULT 9
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 ID AAV68613 standard; cDNA; 1023 BP.

AC AAV68613;
 DT 16-MAR-1999 (first entry)
 XX Human PS116 EST clone 15436711H.
 DE Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 XX detection; therapy; prostate cancer; metastasis; ss.
 KW Homo sapiens.
 XX WO9851805-A1.
 XX 19-NOV-1998.
 XX 15-MAY-1998; 98WO-US010041.
 XX 15-MAY-1997; 97US-00856653.
 XX (ABBO) ABBOTT LAB.
 XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD;
 XX WPI; 1999-045234/04.
 XX New method for detecting diseases of the prostate - comprises use of a
 PT PS116 polynucleotide, protein or antibodies, useful for preventing and

PT treating prostate infections and cancer.
 XX Claim 1; Page 94; 118pp; English.
 CC This sequence represents an expressed sequence tag (EST) clone of the
 CC PS116 gene isolated from a human prostate tissue library. This sequence
 CC can be used in the method of the invention for detecting a target PS116
 CC polynucleotide (PN), that comprises: contacting a sample with at least 1
 CC PS116-specific PN or complement; and detecting the target PS116 PN, where
 CC the specific PN has at least 50% identity with this sequence. The PNs,
 CC PS116 polypeptides or PS116 amplicons are used to detect prostate
 CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
 CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
 CC solid phase. The polypeptides are used for detecting PS116-specific Abs
 CC in a sample, and for producing Abs after immunising a subject. Plasmids
 CC encoding PS116 epitopes can also be administered to a subject to obtain
 CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
 CC staging, monitoring, prognosticating, in vivo imaging, preventing,
 CC treating or determining the predisposition of a subject to diseases and
 CC conditions of the prostate, such as prostate cancer. The Abs and agonists
 CC or inhibitors are useful for treating prostate diseases, tumours and
 CC metastases
 XX
 SQ Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;
 Query Match 100.0%; Score 279; DB 2; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 1.7e-59;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGCCTGCAGCCAG 60
 DB 50 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGCCTGCAGCCAG 109
 QY 61 GCATGCCCCCTGTGCTTACTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 120
 DB 110 GCATGCCCCCTGTGCTTACTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 169
 QY 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 180
 DB 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 229
 QY 181 TCCTGACCGTTCATCAGCAAGAGCTGCACTTGAACCTGGTGATCACTCAGGACTACT 240
 DB 230 TCCTGACCGTTCATCAGCAAGAGCTGCACTTGAACCTGGTGATCACTCAGGACTACT 289
 QY 241 ACGTGGGCAAGAAGACATCAGCTGCTGTGACACCGACT 279
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RESULT 10
 AAV68614
 ID AAV68614 standard; cDNA; 1023 BP.

AC AAV68614;
 XX 16-MAR-1999 (first entry)
 DT Human PS116 EST clone consensus sequence.
 DE Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 KW detection; therapy; prostate cancer; metastasis; ss.
 XX Homo sapiens.
 XX WO9851805-A1.
 XX 19-NOV-1998.
 XX 15-MAY-1998; 98WO-US010041.
 XX 15-MAY-1997; 97US-00856653.
 XX

Db 70 GCAGTGCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 129
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RESULT 14
AAA48374
ID AAA48374 standard; cDNA; 998 BP.
XX
AC AAA48374;
DT 07-SEP-2000 (first entry)
XX
DE Human prostate stem cell antigen, PSCA, coding sequence.
XX
KW Human; prostate cancer; prostate stem cell antigen; PSCA;
KW chromosome 8q24.2; bladder cancer; anti-apoptosis; proliferation;
KW GPI-anchored cell surface antigen; glycosylphosphatidylinositol; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 18..389
FT /*tag= b
FT /product= "Human PSCA"
FT /transl_except= (pos:18..20,aa:Met)
FT /transl_except= (pos:237..239,aa:Ser)
FT sig_peptide 18..77
FT /*tag= a
FT mat_peptide 78..386
FT /*tag= c

WO200032752-A1.
XX
PD 08-JUN-2000.
XX
PF 02-DEC-1999; 99WO-US028883.
XX
PR 02-DEC-1998; 98US-00203939.
PR 17-FEB-1999; 98US-00251835.
PR 25-MAY-1999; 99US-00318503.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Reiter R, Witte O;
XX
DR WPI; 2000-412305/35.
DR P-PSDB; AAY99707.

XX
PT Prostate stem cell antigens, the nucleic acids encoding them and
PT antibodies against them, useful for diagnosing and treating prostate
PT cancer, bladder carcinomas and/or bone metastases of prostate cancer.
XX
PS Claim 28; Fig 1; 171pp; English.

XX
CC The present sequence is the coding sequence for human Prostate Stem Cell
CC Antigen (PSCA). PSCA is a glycosylphosphatidylinositol (GPI)-anchored
CC cell surface antigen, which is expressed across a variety of normal
CC cells: prostate cells, urothelium, renal collecting ducts, colonic
CC neuroendocrine cells, placenta, bladder and ureteral transitional
CC epithelial cells. However, PSCA is widely over-expressed across all
CC stages of prostate cancer, including high grade prostatic intraepithelial
CC neoplasia (PIN), androgen-dependent and androgen-independent prostate

CC tumours and bladder carcinoma. The expression of PSCA appears to
CC correlate with increasing grade and so PSCA may be used as a prostate
CC cancer marker, to discriminate between malignant prostate cancers, normal
CC prostate glands and non-malignant neoplasias. It is hypothesised that
CC PSCA may play a role in stem/progenitor cell function such as self-
CC renewal (anti-apoptosis) and/or proliferation. The PSCA gene has been
CC localised to chromosome 8q24.2. Fragments of the protein encoded by the
CC present sequence (AAY99712, AAY99713 and AAY99714) may be used as
CC antigens to produce antibodies against PSCA. The antibodies may then be
CC used to detect and quantify the presence of PSCA proteins in samples and
CC hence diagnose and prognose prostate cancer. The antibodies may also be
CC used in the treatment of cancers associated with PSCA by inhibiting its
CC expression
XX

SQ Sequence 998 BP; 201 A; 299 C; 286 G; 202 T; 0 U; 10 Other;
Query Match 99.4%; Score 277.4; DB 3; Length 998;
Best Local Similarity 99.6%; Pred. No. 4.1e-59;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTATGGCAGGCTTGCCCTGCAGCCAG 60
Db 10 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTATGGCAGGCTTGCCCTGCAGCCAG 69
Qy 61 GCAGTGCCTGCTGTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 120
Db 70 GCAGTGCCTGCTGTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 129
Qy 121 TGGAGAACTGCAACCCAGCTGGGGAGCAGTGTGACACCGCGCATCCCGCAGTTGGCC 180
Db 130 TGGAGAACTGCAACCCAGCTGGGGAGCAGTGTGACACCGCGCATCCCGCAGTTGGCC 189
Qy 181 TCCTGACCGTTCATCAGCAAGAGCTGCAGCTTGAACCTGCTGGATGACTCAGAGGACTACT 240
Db 190 TCCTGACCGTTCATCAGCAAGAGCTGCAGCTTGAACCTGCTGGATGACTCAGAGGACTACT 249
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Db 250 ACCTGGGCAAGAAATCATCATCTGCTGTGACACCGACT 288

RESULT 15
AAV38061
ID AAV38061 standard; cDNA; 288 BP.
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AC AAV38061;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human stem cell antigen 2 partial sequence from Incyte clone 1312529.
XX
KW Human; stem cell antigen; SCAH-1; SCAH-2; THP-1; bladder tumour;
KW diagnosis; screening; sca-2; LY-6 family; leukaemia; cancer; ss.
XX
OS Homo sapiens.
XX
FN WO9800540-A1.
XX
PD 08-JAN-1998.
XX
PF 25-JUN-1997; 97WO-US010956.
XX
PR 03-JUL-1996; 96US-00675508.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J;
XX
DR WPI; 1998-427478/36.
XX
PT Human stem cell antigens, SCAH-1 and SCAH-2 - useful to, e.g. diagnose
PT and treat SCAH-1 or SCAH-2 related conditions such as tumours and screen
PT inhibitory compounds.

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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 06:05:35 ; Search time 32.5929 Seconds
(without alignments)
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Title: US-09-079-874-3

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/2/ina/PTUS_COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	998	US-09-203-939-1	Sequence 1, Appli
2	279	100.0	998	US-09-251-835-1	Sequence 1, Appli
3	279	100.0	998	US-09-318-503-1	Sequence 1, Appli
4	279	100.0	998	US-09-038-261A-1	Sequence 1, Appli
5	279	100.0	998	US-09-564-329A-1	Sequence 1, Appli
6	277	99.3	288	US-08-675-508-23	Sequence 23, Appl
7	277	99.3	494	US-08-675-508-4	Sequence 4, Appli
8	260	93.2	960	US-09-307-794A-17	Sequence 17, Appl
9	260	93.2	960	US-09-905-125A-17	Sequence 17, Appl
10	260	93.2	960	US-09-902-775A-17	Sequence 17, Appl
11	227	81.4	286	US-08-675-508-21	Sequence 21, Appl
12	218.4	78.3	232	US-08-675-508-25	Sequence 25, Appl
13	148.4	53.2	441	US-09-203-939-3	Sequence 3, Appli
14	148.4	53.2	441	US-09-318-503-3	Sequence 3, Appli
15	148.4	53.2	441	US-09-038-261A-3	Sequence 3, Appli
16	148.4	53.2	441	US-09-564-329A-3	Sequence 3, Appli
17	148.4	53.2	441	US-08-675-508-17	Sequence 17, Appl
18	52.4	18.8	280	US-08-675-508-10	Sequence 10, Appl
19	52.2	18.7	262	US-08-675-508-11	Sequence 11, Appl
20	52.2	18.7	289	US-08-675-508-3	Sequence 3, Appli
21	52.2	18.7	537	US-08-675-508-3	Sequence 3, Appli
22	52.2	18.7	1066	US-08-154-916-1	Sequence 1, Appli
23	52.2	18.7	1095	US-09-139-424-1	Sequence 1, Appli
24	52.2	18.7	1163	US-08-746-397-1	Sequence 1, Appli
25	51.2	18.4	266	US-08-675-508-16	Sequence 16, Appl
26	51.2	18.4	335	US-08-675-508-12	Sequence 12, Appl
27	46.8	16.8	196	US-08-675-508-8	Sequence 8, Appli

28	44.4	15.9	275	2	US-08-675-508-18	Sequence 18, Appli
29	44	15.8	44	4	US-09-907-794A-21	Sequence 21, Appli
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33	43.6	15.6	2805	4	US-09-252-991A-2944	Sequence 2944, Ap
34	43	15.4	1491	4	US-09-252-991A-9935	Sequence 9935, Ap
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38	42.2	15.1	5184	4	US-09-845-583A-9	Sequence 9, Appli
39	42.2	15.1	5184	4	US-09-561-709B-4	Sequence 3324, Ap
40	41.2	14.8	720	4	US-09-252-991A-3324	Sequence 3242, Ap
41	41.2	14.8	1191	4	US-09-252-991A-908	Sequence 908, App
42	38.8	13.9	903	4	US-09-252-991A-1128	Sequence 1128, Ap
43	38.8	13.9	1551	4	US-09-252-991A-4893	Sequence 4893, Ap
44	38.2	13.7	1554	4	US-09-252-991A-4910	Sequence 4910, Ap
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ALIGNMENTS

RESULT 1
US-09-203-939-1
; Sequence 1, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203.939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814.279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071.141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074.675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038.261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
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US-09-203-939-1

Query Match 100.0%; Score 279; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.3e-63;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCACTGCCCTGCTGTCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGG 120
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RESULT 2

US-09-251-835-1
; Sequence 1, Application US/09251835A
; Patent No. 6261789
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US12
; CURRENT APPLICATION NUMBER: US/09/251,835A
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
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; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)

; NAME/KEY: misc feature
; LOCATION: (604)
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; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
US-09-251-835-1

Query Match 100.0%; Score 279; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.3e-63;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTTGATGCGAGGCTTGGCCCTGCAGCCAG 60
DB 10 CAGTGACCATGAAGGCTGTGCTGCTTGCCTTTGATGCGAGGCTTGGCCCTGCAGCCAG 69
QY 61 GCACTGCCCTGCTGTCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGG 120
DB 70 GCACTGCCCTGCTGTCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGG 129
QY 121 TGGAGAACTGCACCCAGCTGGGGAGCGAGTGTGACCCGCGGCATCCGCGAGTTGGCC 180
DB 130 TGGAGAACTGCACCCAGCTGGGGAGCGAGTGTGACCCGCGGCATCCGCGAGTTGGCC 189
QY 181 TCCTGACCGTTCATCAGCAAGGCTGCAGCTTGAATGCGTGTGATGACTCAGAGGACTACT 240
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QY 241 ACCTGGGCAAGAAGAACATCAGCTGCTGTGACACCGACT 279
DB 250 ACCTGGGCAAGAAGAACATCAGCTGCTGTGACACCGACT 288

RESULT 3

US-09-318-503-1
; Sequence 1, Application US/09318503A
; Patent No. 6261791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318,503A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 60/074,675
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835

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Db 130 TGGAGAACTGCAACAGCTGGGGAGCAGTCTGACACCGCGGATCCGGCAGTTGGCC 189
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QY 241 ACGTGGGCAAGAAAGCAATCAGTCTGTGACACCGACT 279
Db 250 ACGTGGGCAAGAAAGCAATCAGTCTGTGACACCGACT 288

RESULT 5

US-09-564-329A-1
; Sequence 1, Application US/09564329A
; Patent No. 6541212
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
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; SEQ ID NO 1
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
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; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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; LOCATION: (615)
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; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-564-329A-1
Query Match 100.0%; Score 279; DB 4; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.3e-63;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGTGACCATGAAGGCTGTGCTTCCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAG 60
Db 10 CAGTGACCATGAAGGCTGTGCTTCCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAG 69
QY 61 GCACCTGCCCTGTGTGCTACTCTCTGAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 120
Db 70 GCACCTGCCCTGTGTGCTACTCTCTGAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 129
QY 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGCATCCCGCAGTTGGCC 180
Db 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGCATCCCGCAGTTGGCC 189
QY 181 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCACAGGACTACT 240
Db 190 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCACAGGACTACT 249
QY 241 ACGTGGGCAAGAAAGCAATCAGTCTGTGACACCGACT 279
Db 250 ACGTGGGCAAGAAAGCAATCAGTCTGTGACACCGACT 288

RESULT 6

US-08-675-508-23
; Sequence 23, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,508
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
IMMEDIATE SOURCE:
LIBRARY: BLADTUT02
CLONE: 1312529
US-08-675-508-23

Query Match 99.3%; Score 277; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.6e-63;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGACCATGAAGGCTGTGCTTGCCTTGTGAGGAGGCTTGGCCCTGCAGCCAGGC 62
DB 1 GTGACCATGAAGGCTGTGCTTGCCTTGTGAGGAGGCTTGGCCCTGCAGCCAGGC 60
QY 63 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTCCCTGCAGGTG 122
DB 61 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTCCCTGCAGGTG 120
QY 123 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGCAACCGCGGATCCGCGCAGTTGGCCTC 182
DB 121 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGCAACCGCGGATCCGCGCAGTTGGCCTC 180
QY 183 CTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGCTGGATGACTCACAGGACTACTAC 242
DB 181 CTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGCTGGATGACTCACAGGACTACTAC 240
QY 243 GTGGGCAAGAAGAACATCATCAGCTGTGTGACACCGACT 279
DB 241 GTGGGCAAGAAGAACATCATCAGCTGTGTGACACCGACT 277

RESULT 8
US-09-907-794A-17
Sequence 17, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26

TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
IMMEDIATE SOURCE:
LIBRARY: BLADTUT02
CLONE: 1312529
US-08-675-508-23

Query Match 99.3%; Score 277; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.6e-63;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGACCATGAAGGCTGTGCTTGCCTTGTGAGGAGGCTTGGCCCTGCAGCCAGGC 62
DB 1 GTGACCATGAAGGCTGTGCTTGCCTTGTGAGGAGGCTTGGCCCTGCAGCCAGGC 60
QY 63 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTCCCTGCAGGTG 122
DB 61 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTCCCTGCAGGTG 120
QY 123 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGCAACCGCGGATCCGCGCAGTTGGCCTC 182
DB 121 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGCAACCGCGGATCCGCGCAGTTGGCCTC 180
QY 183 CTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGCTGGATGACTCACAGGACTACTAC 242
DB 181 CTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGCTGGATGACTCACAGGACTACTAC 240
QY 243 GTGGGCAAGAAGAACATCATCAGCTGTGTGACACCGACT 279
DB 241 GTGGGCAAGAAGAACATCATCAGCTGTGTGACACCGACT 277

RESULT 7
US-08-675-508-4
Sequence 4, Application US/08675508
Patent No. 5856136
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0066 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

/ PRIOR APPLICATION NUMBER: US 60/146,222
 / PRIOR FILING DATE: 1999-07-28
 / PRIOR APPLICATION NUMBER: PCT/US99/20594
 / PRIOR FILING DATE: 1999-09-08
 / PRIOR APPLICATION NUMBER: PCT/US99/20944
 / PRIOR FILING DATE: 1999-09-13
 / PRIOR APPLICATION NUMBER: PCT/US99/21090
 / PRIOR FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: PCT/US99/21547
 / PRIOR FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: PCT/US99/23089
 / PRIOR FILING DATE: 1999-10-05
 / PRIOR APPLICATION NUMBER: PCT/US99/28214
 / PRIOR FILING DATE: 1999-11-29
 / PRIOR APPLICATION NUMBER: PCT/US99/28313
 / PRIOR FILING DATE: 1999-11-30
 / PRIOR APPLICATION NUMBER: PCT/US99/28564
 / PRIOR FILING DATE: 1999-12-02
 / PRIOR APPLICATION NUMBER: PCT/US99/28565
 / PRIOR FILING DATE: 1999-12-02
 / PRIOR APPLICATION NUMBER: PCT/US99/30095
 / PRIOR FILING DATE: 1999-12-16
 / PRIOR APPLICATION NUMBER: PCT/US99/30911
 / PRIOR FILING DATE: 1999-12-20
 / PRIOR APPLICATION NUMBER: PCT/US99/30999
 / PRIOR FILING DATE: 1999-12-20
 / PRIOR APPLICATION NUMBER: PCT/US00/00219
 / PRIOR FILING DATE: 2000-01-05
 / NUMBER OF SEQ ID NOS: 423
 / SEQ ID NO 17
 / LENGTH: 960
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-09-907-794A-17

Query Match 93.2%; Score 260; DB 4; Length 960;
 Best Local Similarity 100.0%; Pred. No. 1.9e-58;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	20	GCTGCTTGCCTTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTA	79
Db	1	GCTGCTTGCCTTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTA	60
QY	80	CTCCTGCAAGCCAGGTCAGCAACGAGGACTGCTGTCAGGTGGAGAACTGCACCCAGCT	139
Db	61	CTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGTCAGGTGGAGAACTGCACCCAGCT	120
QY	140	GGGGAGAGCTGCTGGACCGCCGATCGGCGAGTTGGCTCTCTGACCGTCATCAGCA	199
Db	121	GGGGAGAGCTGCTGGACCGCCGATCGGCGAGTTGGCTCTCTGACCGTCATCAGCA	180
QY	200	AGGCTCAGCTTGAATCGGTGGATGACTCAGGAGTACTACGCTGGGCAAGAGAACAT	259
Db	181	AGGCTCAGCTTGAATCGGTGGATGACTCAGGAGTACTACGCTGGGCAAGAGAACAT	240
QY	260	CACGTGCTGTGACCCGACT 279	
Db	241	CACGTGCTGTGACCCGACT 260	

RESULT 9
 US-09-905-125A-17
 / Sequence 17, Application US/09905125A
 / Patent No. 6664376
 / GENERAL INFORMATION:
 / APPLICANT: Genentech, Inc.
 / APPLICANT: Ashkenazi, Avi
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman

/ APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, A.
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, Christopher J.
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth, J.
 / APPLICANT: Kijavini, Ivar J.
 / APPLICANT: Kijavini, Jennie P.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Thomas, Daniel
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William, I.
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / TITLE OF INVENTION: Acids Encoding the Same
 / FILE REFERENCE: 10466-14
 / CURRENT APPLICATION NUMBER: US/09/905,125A
 / CURRENT FILING DATE: 2001-07-12
 / PRIOR APPLICATION NUMBER: PCT/US00/04414
 / PRIOR FILING DATE: 2000-02-22
 / PRIOR APPLICATION NUMBER: US 60/143,048
 / PRIOR FILING DATE: 1999-07-07
 / PRIOR APPLICATION NUMBER: US 60/145,698
 / PRIOR FILING DATE: 1999-07-26
 / PRIOR APPLICATION NUMBER: US 60/146,222
 / PRIOR FILING DATE: 1999-07-28
 / PRIOR APPLICATION NUMBER: PCT/US99/20594
 / PRIOR FILING DATE: 1999-09-08
 / PRIOR APPLICATION NUMBER: PCT/US99/20944
 / PRIOR FILING DATE: 1999-09-13
 / PRIOR APPLICATION NUMBER: PCT/US99/21090
 / PRIOR FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: PCT/US99/21547
 / PRIOR FILING DATE: 1999-09-15
 / PRIOR APPLICATION NUMBER: PCT/US99/23089
 / PRIOR FILING DATE: 1999-10-05
 / PRIOR APPLICATION NUMBER: PCT/US99/28214
 / PRIOR FILING DATE: 1999-11-29
 / PRIOR APPLICATION NUMBER: PCT/US99/28313
 / PRIOR FILING DATE: 1999-11-30
 / PRIOR APPLICATION NUMBER: PCT/US99/28564
 / PRIOR FILING DATE: 1999-12-02
 / PRIOR APPLICATION NUMBER: PCT/US99/28565
 / PRIOR FILING DATE: 1999-12-02
 / PRIOR APPLICATION NUMBER: PCT/US99/30095
 / PRIOR FILING DATE: 1999-12-16
 / PRIOR APPLICATION NUMBER: PCT/US99/30911
 / PRIOR FILING DATE: 1999-12-20
 / PRIOR APPLICATION NUMBER: PCT/US99/30999
 / PRIOR FILING DATE: 1999-12-20
 / PRIOR APPLICATION NUMBER: PCT/US00/00219
 / PRIOR FILING DATE: 2000-01-05
 / NUMBER OF SEQ ID NOS: 423
 / SEQ ID NO 17
 / LENGTH: 960
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-09-907-794A-17

Query Match 93.2%; Score 260; DB 4; Length 960;
 Best Local Similarity 100.0%; Pred. No. 1.9e-58;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	20	GCTGCTTGCCTTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTA	79
Db	1	GCTGCTTGCCTTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTA	60
QY	80	CTCCTGCAAGCCAGGTCAGCAACGAGGACTGCTGTCAGGTGGAGAACTGCACCCAGCT	139
Db	61	CTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGTCAGGTGGAGAACTGCACCCAGCT	120
QY	140	GGGGAGAGCTGCTGGACCGCCGATCGGCGAGTTGGCTCTCTGACCGTCATCAGCA	199
Db	121	GGGGAGAGCTGCTGGACCGCCGATCGGCGAGTTGGCTCTCTGACCGTCATCAGCA	180
QY	200	AGGCTCAGCTTGAATCGGTGGATGACTCAGGAGTACTACGCTGGGCAAGAGAACAT	259
Db	181	AGGCTCAGCTTGAATCGGTGGATGACTCAGGAGTACTACGCTGGGCAAGAGAACAT	240
QY	260	CACGTGCTGTGACCCGACT 279	
Db	241	CACGTGCTGTGACCCGACT 260	

RESULT 9
 US-09-905-125A-17
 / Sequence 17, Application US/09905125A
 / Patent No. 6664376
 / GENERAL INFORMATION:
 / APPLICANT: Genentech, Inc.
 / APPLICANT: Ashkenazi, Avi
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman

Db 61 CTCCTGCAAGCCAGGTAGCAACGAGGAGCTGCTGCGAGTGGAGAACTGCACCCAGCT 120
Qy 140 GGGGAGCAGTGTGGACCGCGCATCCGGCGAGTTGGCTCTCTGACCGTGCATCAGCAA 199
Db 121 GGGGAGCAGTGTGGACCGCGCATCCGGCGAGTTGGCTCTCTGACCGTGCATCAGCAA 180
Qy 200 AGGCTGACGTTGAATGCTGGATGATCTACAGCACTATCTACGTTGGCGAAGAGAACAT 259
Db 181 AGGCTGACGTTGAATGCTGGATGATCTACAGCACTATCTACGTTGGCGAAGAGAACAT 240
Qy 260 CACGTGCTGTGACACCGGACT 279
Db 241 CACGTGCTGTGACACCGGACT 260

RESULT 10
US-09-902-775A-17
; Sequence 17, Application US/09902775A
; Patent No. 6866451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-17
Query Match 93.2%; Score 260; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.9e-58;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 GCTGCTGGCCCTGTTGATGGCAGGCTTGGCCCTGACCCAGGACTGCCCTGCTGTGCTA 79
Db 1 GCTGCTGGCCCTGTTGATGGCAGGCTTGGCCCTGACCCAGGACTGCCCTGCTGTGCTA 60
Qy 80 CTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGGTGGAGAACTGCACCCAGCT 139
Db 61 CTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGGTGGAGAACTGCACCCAGCT 120
Qy 140 GGGGAGCAGTGTGACACCGCGCATCCGGCGAGTTGGCTCTCTGACCGTGCATCAGCAA 199
Db 121 GGGGAGCAGTGTGACACCGCGCATCCGGCGAGTTGGCTCTCTGACCGTGCATCAGCAA 180
Qy 200 AGGCTGACGTTGAATGCTGGATGATCTACAGCACTATCTACGTTGGCGAAGAGAACAT 259
Db 181 AGGCTGACGTTGAATGCTGGATGATCTACAGCACTATCTACGTTGGCGAAGAGAACAT 240
Qy 260 CACGTGCTGTGACACCGGACT 279
Db 241 CACGTGCTGTGACACCGGACT 260

RESULT 11
US-09-675-508-21
; Sequence 21, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,508
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

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; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 286 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; LIBRARY: UTRSNOT01
; CLONE: 588615
; US-08-675-508-21

Query Match      81.4%; Score 227; DB 2; Length 286;
Best Local Similarity 97.5%; Pred. No. 4.8e-50;
Matches 238; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 36 ATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCCCTGCTGTGCTACTCTCTGCAAAAGCCGAG 95
Db 1 ATGGCAGGCTTGGCCCTGCGAGCCAGGCACTGCCCTGCTGTGCTACTCTCTGCAAAAGCCGAG 60
QY 96 GTGAGCAACGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGG 155
Db 61 GTGAGCAACGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGG 120
QY 156 ACCGGCGCATCCGCGCAGTTGGCTCTCTGAGCACTGACCGTTCATCAGCAAGGCTGCAGCTTGAC 215
Db 121 ACCGGCGCATCCGCGCAGTTGGCTCTCTGAGCACTGACCGTTCATCAGCAAGGCTGCAGCTTGAC 179
QY 216 TGCCTGGTGAATCAGCAGGACTACTACCTGGGCAAGAAAGAAATCAGCAGTGTGTGACACC 275
Db 180 TGCCTGGTGAATCAGCAGGACTACTACCTGGGCAAGAAAGAAATCAGCAGTGTGTGACACC 239
QY 276 GACT 279
Db 240 GACT 243

RESULT 12
US-08-675-508-25
; Sequence 25, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,508
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 232 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
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; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT02
; CLONE: 1315052
; US-08-675-508-25

Query Match      78.3%; Score 218.4; DB 2; Length 232;
Best Local Similarity 99.1%; Pred. No. 7.6e-48;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 4 TGACCATGAGGCTGTGCTGTGCTTGGCCCTGTGATGCGAGGCTTGGCCCTGCGAGCCAGGCA 63
Db 1 TGACCATGAGGCTGTGCTGTGCTTGGCCCTGTGATGCGAGGCTTGGCCCTGCGAGCCAGGCA 60
QY 64 CTGCCCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTCCCTGCGAGGTGG 123
Db 61 CTGCCCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTCCCTGCGAGGTGG 120
QY 124 AGAAGTGCACCCAGCTGGGGGAGCAGTGTGACACCGCGGCATCCGCGAGTTGGCTTCC 183
Db 121 AGAAGTGCACCCAGCTGGGGGAGCAGTGTGACACCGCGGCATCCGCGAGTTGGCTTCC 180
QY 184 TGACCCGTTCATCAGC-AAAGGCTGCGAGCTTGAACCTGCGTGGATGACTCACAGG 234
Db 181 TGACCCGTTCATCACAAGAGGCTGCGAGCTTGAACCTGCGTGGATGACTCACAGG 232

RESULT 13
US-09-203-939-3
; Sequence 3, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)
; US-09-203-939-3

Query Match      53.2%; Score 148.4; DB 3; Length 441;
Best Local Similarity 71.9%; Pred. No. 1.1e-29;
Matches 194; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 9 ATGAGGCTGTGCTGTGCTTGGCCCTGTGATGCGAGGCTTGGCCCTGCGAGCCAGGCACTGCC 68
Db 1 ATGAGAGACAGTTTTTTTTTATCTGCTGTGCGCACCTACTTAGCCCTGCATCCAGGTGCTGCT 60
QY 69 CTGCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTTCAAGTGGAGAAC 128
Db 61 CTGCACTGTCTATTCTATGCAACAGACAGATGAACAACAGAGACTGTCTGAATGTACAGAAC 120
QY 129 TGCACCCAGCTGGGGGAGCAGTGTGACACCGCGGCATCCGCGAGTTGGCTTCTGCTGACC 188
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QY 189 GTCATCAGCAAAAGGCTGCGAGCTTGAACCTGCGTGGATGACTCACAGGACTACTACGTGGGC 248
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249 AAGAAGACATCATCGTGTGACACCGAC 278
241 AAGAAGACATCATCGTGTGACACCGAC 270

RESULT 14
US-09-251-835-3
Sequence 3, Application US/09251835A
Patent No. 6261789
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
FILE REFERENCE: 30435.54US12
CURRENT APPLICATION NUMBER: US/09/251,835A
CURRENT FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 441
TYPE: DNA
ORGANISM: MURINE PSCA (mpSCA)
US-09-318-503-3

Query Match 53.2%; Score 148.4; DB 3; Length 441;
Best Local Similarity 71.9%; Pred. No. 1.1e-29;
Matches 194; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 9 ATGAAGGCTGTGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCC 68
Db 1 ATGAAGACAGTTTTTTTATCTCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT 60
QY 69 CTGCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGAGGTGGAGAAC 128
Db 61 CTGCAAGTCTATTTCATGCACAGCAGATGAAACACAGAGACTGTCTGAATGTACAGAAC 120
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Db 121 TGCAGCTGACACGACAGTGTGCTTTACATCGGCGCATCCGGGCCATTGGACTCGTGACA 180
QY 189 GTCATCAGCAAGGCTGCAGCTTGAACCTGCTGGATGACTCAGGACTACTACGTGGGC 248
Db 181 GTTATCAGTAAGGCTGCAGCTCAGCTCAGCTGTCAGGATGACTCGGAGAACTACTATTGGGC 240
QY 249 AAGAAGACATCATCGTGTGACACCGAC 278
Db 241 AAGAAGACATCATCGTGTGACACCGAC 270

Search completed: September 18, 2004, 19:23:18
Job time : 33.5929 secs

249 AAGAAGACATCATCGTGTGACACCGAC 278
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RESULT 15
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Sequence 3, Application US/09318503A
Patent No. 6261791
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US13
CURRENT APPLICATION NUMBER: US/09/318,503A
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 08/814,279
EARLIER FILING DATE: 1997-03-10

Query Match 53.2%; Score 148.4; DB 3; Length 441;
Best Local Similarity 71.9%; Pred. No. 1.1e-29;
Matches 194; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 9 ATGAAGGCTGTGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCC 68
Db 1 ATGAAGACAGTTTTTTTATCTCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT 60
QY 69 CTGCTGTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGAGGTGGAGAAC 128
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Db 121 TGCAGCTGACACGACAGTGTGCTTTACATCGGCGCATCCGGGCCATTGGACTCGTGACA 180
QY 189 GTCATCAGCAAGGCTGCAGCTTGAACCTGCTGGATGACTCAGGACTACTACGTGGGC 248
Db 181 GTTATCAGTAAGGCTGCAGCTCAGCTCAGCTGTCAGGATGACTCGGAGAACTACTATTGGGC 240
QY 249 AAGAAGACATCATCGTGTGACACCGAC 278
Db 241 AAGAAGACATCATCGTGTGACACCGAC 270

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 06:17:58 ; Search time 209.097 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	279	100.0	990	13	US-10-240-425-386
3	279	100.0	990	15	US-10-117-937-87
4	279	100.0	990	17	US-10-188-832-168
5	279	100.0	998	9	US-09-564-329A-1
6	279	100.0	998	9	US-08-B55-453-1
7	279	100.0	998	9	US-08-854-811-1
8	279	100.0	998	9	US-09-934-773-1
9	279	100.0	998	9	US-09-943-620-1
10	279	100.0	998	10	US-09-855-632-1
11	279	100.0	998	15	US-10-225-784-1
12	279	100.0	998	15	US-10-224-720-1
13	279	100.0	998	15	US-10-325-779-1
14	279	100.0	998	16	US-10-374-381-1

ALIGNMENTS

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RESULT 1
US-09-080-140-3
Sequence 3, Application US/09080140
Publication No. US2004018553A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
SHEET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,140
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

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QY 121 TGGAGAACTGACCCAGCTGGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 180
Db 130 TGGAGAACTGACCCAGCTGGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 189
QY 131 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 240
Db 130 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 249
QY 241 ACGTGGGCAAGAAGAACATCATCGTCTGTGACACCGACT 279
Db 250 ACGTGGGCAAGAAGAACATCATCGTCTGTGACACCGACT 288

RESULT 4
US-10-188-832-168
Sequence 168, Application US/10188832
Publication No. US20040076955A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Azi, Natasha
TITLE OF INVENTION: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: And Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 168
LENGTH: 990
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (1)-(990)
OTHER INFORMATION: n = g, a, c or t
US-10-188-832-168

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Best Local Similarity 100.0%; Pred. No. 3.6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGCTCTGCTTGCCTTGTGATGCAGGCTTGGCCCTGCAGCCAG 60
Db 10 CAGTGACCATGAAGGCTGCTCTGCTTGCCTTGTGATGCAGGCTTGGCCCTGCAGCCAG 59
QY 61 GCAGTGCCTGCTGCTGCTACTCTCTGCAAGCCAGGCTGAGCAACGAGGACTGCTGCAGG 120
Db 70 GCAGTGCCTGCTGCTGCTACTCTCTGCAAGCCAGGCTGAGCAACGAGGACTGCTGCAGG 129
QY 121 TGGAGAACTGACCCAGCTGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 180
Db 130 TGGAGAACTGACCCAGCTGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCC 189
QY 181 TCCTGACCGTCTATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACT 240
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QY 241 ACGTGGGCAAGAAGAACATCATCGTCTGTGACACCGACT 279
Db 250 ACGTGGGCAAGAAGAACATCATCGTCTGTGACACCGACT 288

RESULT 5
US-09-564-329A-1
Sequence 1, Application US/09564329A
Patent No. US20010055751A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/564,329A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 998
TYPE: DNA
ORGANISM: HUMAN PSMA (hPSCA)
FEATURE:
NAME/KEY: misc feature
LOCATION: (543)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (580)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (584)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (604)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (608)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (615)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (636)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (640)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (646)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
NAME/KEY: misc feature
LOCATION: (697)
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NAME/KEY: misc feature


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Query Match      100.0%; Score 279; DB 9; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGTGACCATGAAGGCTGTGCTCTTGGCCCTGTGTGATGCGAGGCTTGGCCCTGACGCCAG 60
Db 10 CAGTGACCATGAAGGCTGTGCTCTTGGCCCTGTGTGATGCGAGGCTTGGCCCTGACGCCAG 69
Qy 61 GCACTGCCCTGTGCTCTTCTCTCTCAAGAGCCAGGTGAGCAACGAGAGCTCCCTGCGAGG 120
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Qy 181 TCTGACCGTCTACACAAAGGCTGCGCTTGAATCGGTGATGACTACACAGGACTACT 240
Db 190 TCTGACCGTCTACACAAAGGCTGCGCTTGAATCGGTGATGACTACACAGGACTACT 249
Qy 241 ACCTGGGCAAGAGACATCAGTGTCTGTGACACCGACT 279
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RESULT 9

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US-09-963-620-1
; Sequence 1, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
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; LOCATION: (543)
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; NAME/KEY: misc_feature

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; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (604)
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; NAME/KEY: misc_feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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Query Match 100.0%; Score 279; DB 9; Length 998;

Best Local Similarity 100.0%; Pred. No. 3.6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CAGTGACCATGAAGGCTGTGCTCTTGGCCCTGTGTGATGCGAGGCTTGGCCCTGACGCCAG 60
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Qy 121 TGGAGAACTGCAACCCAGCTGGGGAGCAGTGTGACACCGCGCATCGCGCAGTTGCC 180
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RESULT 10

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; Publication No. US20030113818A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,632
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279

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/ PRIOR APPLICATION NUMBER: 60/071,141
/ PRIOR FILING DATE: 1998-01-12
/ PRIOR APPLICATION NUMBER: 60/074,675
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: 60/113,230
/ PRIOR FILING DATE: 1998-12-21
/ PRIOR APPLICATION NUMBER: 60/120,536
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 60/124,658
/ PRIOR FILING DATE: 1999-03-16
/ PRIOR APPLICATION NUMBER: 09/038,261
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 09/203,939
/ PRIOR FILING DATE: 1998-12-02
/ PRIOR APPLICATION NUMBER: 09/251,835
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 09/308,503
/ PRIOR FILING DATE: 1999-03-25
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 998
/ TYPE: DNA
/ ORGANISM: HUMAN PSCA (hPSCA)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (543)
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
/ NAME/KEY: misc_feature
/ LOCATION: (580)
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
/ NAME/KEY: misc_feature
/ LOCATION: (584)
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
/ NAME/KEY: misc_feature
/ LOCATION: (604)
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/ LOCATION: (646)
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/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ US-09-855-632-1
Query Match 100.0%; Score 279; DB 10; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGTGACCATCAAGCGTGTGCTTGCCTGTGATGGCAGGCTGGCCCTGCAGCCAG 60
Db 10 CAGTGACCATCAAGCGTGTGCTTGCCTGTGATGGCAGGCTGGCCCTGCAGCCAG 69
QY 61 GCAGTGCCTGTGTGTACTCTTCGAAAGCCAGGAGTGCACGAGGACTGCTGCAGG 120
Db 70 GCAGTGCCTGTGTGTACTCTTCGAAAGCCAGGAGTGCACGAGGACTGCTGCAGG 129

121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCCCGCAGTTGGCC 180
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181 TCCTGACCGTCAATCAGCAAAAGGCTGCAGCTTGAACCTGGTGGATGACTACAGGACTACT 240
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250 ACCTGGCAGAGAAACATCAGCTGTGTGACACCGACT 288

RESULT 11
US-10-225-784-1
/ Sequence 1, Application US/10225784
/ Publication No. US20030113820A1
/ GENERAL INFORMATION:
/ APPLICANT: Reiter, Robert E.
/ APPLICANT: Witte, Owen N.
/ APPLICANT: Saffran, Douglas C.
/ TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
/ FILE REFERENCE: 30435.54US14
/ CURRENT APPLICATION NUMBER: US/10/225,784
/ CURRENT FILING DATE: 2002-08-21
/ PRIOR APPLICATION NUMBER: US/09/564,329
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: 09/359,326
/ PRIOR FILING DATE: 1999-07-20
/ PRIOR APPLICATION NUMBER: 03/814,279
/ PRIOR FILING DATE: 1997-03-10
/ PRIOR APPLICATION NUMBER: 60/071,141
/ PRIOR FILING DATE: 1998-01-12
/ PRIOR APPLICATION NUMBER: 60/074,675
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: 60/113,230
/ PRIOR FILING DATE: 1998-12-21
/ PRIOR APPLICATION NUMBER: 60/120,536
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 60/124,658
/ PRIOR FILING DATE: 1999-03-16
/ PRIOR APPLICATION NUMBER: 09/038,261
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 09/203,939
/ PRIOR FILING DATE: 1998-12-02
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patent In Ver. 2.0
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/ LENGTH: 998
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (543)
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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/ NAME/KEY: misc_feature
/ LOCATION: (580)
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (584)
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (604)
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (608)
/ OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
/ FEATURE:
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NAME/KEY: misc feature
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OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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NAME/KEY: misc feature
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OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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NAME/KEY: misc feature
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FEATURE:
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NAME/KEY: misc feature
LOCATION: (697)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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NAME/KEY: misc feature
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US-10-225-784-1

Query Match 100.0%; Score 279; DB 15; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTGATGGCAGGCTGGCCCTGCAGCCAG 60
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QY 181 TCTGACCTGTATCAGCAAGCTGCAGCTTGAACCTGGTGTGATCACTCAGAGGACTACT 240
DB 190 TCTGACCTGTATCAGCAAGCTGCAGCTTGAACCTGGTGTGATCACTCAGAGGACTACT 249

QY 241 ACCTGGGCAAGAAACATCACGTGCTGTGACACCGACT 279
DB 250 ACCTGGGCAAGAAACATCACGTGCTGTGACACCGACT 288

RESULT 12
US-10-224-720-1
Sequence 1, Application US/10224720
Publication No. US20030147806A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/10/224,720
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US/09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536

PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 998
TYPE: DNA
ORGANISM: HUMAN PSCA (hPSCA)
FEATURE:
NAME/KEY: misc feature
LOCATION: (543)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
FEATURE:
NAME/KEY: misc feature
LOCATION: (580)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
FEATURE:
NAME/KEY: misc feature
LOCATION: (584)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
FEATURE:
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LOCATION: (604)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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LOCATION: (608)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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NAME/KEY: misc feature
LOCATION: (926)
OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-10-224-720-1

Query Match 100.0%; Score 279; DB 15; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTGATGGCAGGCTGGCCCTGCAGCCAG 60
DB 10 CAGTGACCATGAAGCTGTGCTGCTTGCCTTGTGATGGCAGGCTGGCCCTGCAGCCAG 69

QY 61 GCACCTCCCTGTGCTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 120
DB 70 GCACCTCCCTGTGCTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCCTGCAGG 129


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QY 121 TGGAGAACTGCACCCAGCTGGGGAGAGTGTGTGACCGCGGCATCCGCGCAGTTGGCC 180
Db 130 TGGAGAACTGCACCCAGCTGGGGAGAGTGTGTGACCGCGGCATCCGCGCAGTTGGCC 189
QY 181 TCTGACCGTCTATCAGCAAGGCTCAGCTTGAATGGTGGTGAATCAACAGGACTACT 240
Db 190 TCTGACCGTCTATCAGCAAGGCTCAGCTTGAATGGTGGTGAATCAACAGGACTACT 249
QY 241 ACCTGGGCAAGAGAACATCATCGTGTGTGACACCGACT 279
Db 250 ACCTGGGCAAGAGAACATCATCGTGTGTGACACCGACT 288

RESULT 13
US-10-225-779-1
; Sequence 1, Application US/10225779
; Publication No. US20030153016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
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; US-10-225-779-1

Query Match 100.0%; Score 279; DB 15; Length 998;
Best Local Similarity 100.0%; Pred. No. 3.6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCAG 60
Db 10 CAGTGACCATGAAGGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCAG 69
QY 61 GCATCTGCCCTGCTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCAG 120
Db 70 GCATCTGCCCTGCTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCAG 129
QY 121 TGGAGAACTGCACCCAGCTGGGGAGAGTGTGTGACCGCGGCATCCGCGCAGTTGGCC 180
Db 130 TGGAGAACTGCACCCAGCTGGGGAGAGTGTGTGACCGCGGCATCCGCGCAGTTGGCC 189
QY 181 TCCTGACCGTCTATCAGCAAGGCTCAGCTTGAATGGTGGTGAATCAACAGGACTACT 240
Db 190 TCCTGACCGTCTATCAGCAAGGCTCAGCTTGAATGGTGGTGAATCAACAGGACTACT 249
QY 241 ACCTGGGCAAGAGAACATCATCGTGTGTGACACCGACT 279
Db 250 ACCTGGGCAAGAGAACATCATCGTGTGTGACACCGACT 288

RESULT 14
US-10-374-381-1
; Sequence 1, Application US/10374381
; Publication No. US20030228318A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/374,381
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/564,329A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
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; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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US-10-446-542-1

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Best Local Similarity 100.0%; Pred. No. 3,6e-74;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      70  GCACTGCCCTGTGCTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGG 129

QY      121  TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCCGCGCATCCGCGAGTTGGCC 180
Db      130  TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCCGCGCATCCGCGAGTTGGCC 189

QY      181  TCCTGACCGTCAATCAGCAAGGCTGCAGCTTGAATGCGTGGATGACTCAGGACTACT 240
Db      190  TCCTGACCGTCAATCAGCAAGGCTGCAGCTTGAATGCGTGGATGACTCAGGACTACT 249

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-079-874-3

Perfect score: 279
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	279	100.0	480	12	BM819937
4	279	100.0	527	13	BQ083498

5	279	100.0	550	14	CB147558
6	279	100.0	827	12	BM018750
7	279	100.0	942	12	BM018834
8	277.4	99.4	947	12	BM228076
9	277.4	99.4	820	14	CB996183
10	277.4	99.4	843	14	CB997275
11	277.4	99.4	851	14	CB993163
12	277	99.3	682	12	BM042219
13	277	99.3	692	12	BM042219
14	277	99.3	1024	8	BC023582
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33	185	66.3	911	13	BM194301
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36	153	54.8	642	12	BI253941
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ALIGNMENTS

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DEFINITION linear mRNA EST 04-MAR-2002
ACCESSION BM768967
VERSION BM768967.1 GI:19098582
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 424)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 13 row: D column: 04
High quality sequence stop: 424.

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BC048808 Homo sapi
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BQ678675 AGENCOURT
BQ876328 AGENCOURT
BM179764 AGENCOURT
AY418122 Homo sapi
BM173702 AGENCOURT
BM168445 AGENCOURT
BI763453 603047463
BM765417 602738887
BM157227 AGENCOURT
BQ680817 AGENCOURT
AY418123 Pan trogl
BM041997 603615850
BM168360 AGENCOURT
BM38702 AGENCOURT
BM194301 AGENCOURT
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BQ230697 AGENCOURT

FEATURES
source

Location/Qualifiers
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/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 279; DB 12; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTTGGCCCTTTGATGCGAGGCTTGCCCTTGACGCCAG 60
Db 50 CAGTGACCATGAAGGCTGTGCTTGGCCCTTTGATGCGAGGCTTGCCCTTGACGCCAG 109
QY 61 GCAGTGCCTCTGTGCTTACTCTCCAAAGCCAGGTGAGCAACGAGGACTGCCTTGCGAGG 120
Db 110 GCAGTGCCTCTGTGCTTACTCTCCAAAGCCAGGTGAGCAACGAGGACTGCCTTGCGAGG 169
QY 121 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCC 180
Db 170 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCC 229
QY 181 TCCTGACCGTCAACGAAAGCTGCAGCTTGAATCGGTGATGACTCAGAGGACTACT 240
Db 230 TCCTGACCGTCAACGAAAGCTGCAGCTTGAATCGGTGATGACTCAGAGGACTACT 289
QY 241 ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGACT 279
Db 290 ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGACT 328

RESULT 2

BQ083505
LOCUS
DEFINITION K-EST0146186 S14K402 Homo sapiens cDNA clone S14K402-65-D08 5', mRNA linear EST 04-APR-2002
rna sequence.

ACCESSION BQ083505
VERSION BQ083505.1 GI:19942340
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 470)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 65 row: D column: 08

High quality sequence step: 470.

FEATURES

source

1..470
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="S14K402-65-D08"
/cell_line="K402"
/lab_host="Top10F"
/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 279; DB 13; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.9e-49;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTTGGCCCTTTGATGCGAGGCTTGCCCTTGACGCCAG 60
Db 50 CAGTGACCATGAAGGCTGTGCTTGGCCCTTTGATGCGAGGCTTGCCCTTGACGCCAG 109
QY 61 GCAGTGCCTCTGTGCTTACTCTCCAAAGCCAGGTGAGCAACGAGGACTGCCTTGCGAGG 120
Db 110 GCAGTGCCTCTGTGCTTACTCTCCAAAGCCAGGTGAGCAACGAGGACTGCCTTGCGAGG 169
QY 121 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCC 180
Db 170 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCGCATCCGCGCAGTTGGCC 229
QY 181 TCCTGACCGTCAACGAAAGCTGCAGCTTGAATCGGTGATGACTCAGAGGACTACT 240
Db 230 TCCTGACCGTCAACGAAAGCTGCAGCTTGAATCGGTGATGACTCAGAGGACTACT 289
QY 241 ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGACT 279
Db 290 ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGACT 328

RESULT 3

BQ083505

LOCUS

DEFINITION K-EST0088167 S18N69761 Homo sapiens cDNA clone S18N69761-19-E04

5', mRNA sequence.

ACCESSION BQ083505

VERSION BQ083505.1 GI:19176350

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 480)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

```

Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 19, Row: E column: 04
High quality sequence stop: 480.
Location/Qualifiers
1. .480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-19-E04"
/sex="F"
/lab_host="Top10F"
/lab_lib="S18N669761"
/notes="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 100.0%; Score 279; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.9e-49;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGTGACCATGAAGGCTGCTCTTCCCTGTTGATGCGAGGCTTGGCCCTGCAGCCAG 60
Db 10 CAGTGACCATGAAGGCTGCTCTTCCCTGTTGATGCGAGGCTTGGCCCTGCAGCCAG 69
Qy 61 GCAGTGCCCTGCTGTGCTACTCTCTGCAAGCCGAGGTGAGCAACGAGGACTGCTGCAGG 120
Db 70 GCAGTGCCCTGCTGTGCTACTCTCTGCAAGCCGAGGTGAGCAACGAGGACTGCTGCAGG 129
Qy 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 180
Db 130 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 189
Qy 181 TCCTGACCGTCATCAGCAAGGCTGCAGTTGACCTGCGTGGATGACTCAGAGGACTACT 240
Db 190 TCCTGACCGTCATCAGCAAGGCTGCAGTTGACCTGCGTGGATGACTCAGAGGACTACT 249
Qy 241 ACCTGGGCAAGAAGAACATCACGTGCTGTGACACCGACT 279
Db 250 ACCTGGGCAAGAAGAACATCACGTGCTGTGACACCGACT 288

RESULT 4
BQ083498
LOCUS
DEFINITION
K-EST0146178 S14K402 Homo sapiens cDNA clone S14K402-65-C11 5',
mRNA sequence.
ACCESSION
BQ083498
VERSION
BQ083498.1 GI:19942325
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 19, Row: E column: 04
High quality sequence stop: 480.
Location/Qualifiers
1. .527
/organism="Homo sapiens"
/mol_type="mRNA"
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/cell_line="K402"
/lab_host="Top10F"
/lab_lib="S14K402"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 100.0%; Score 279; DB 13; Length 527;
Best Local Similarity 100.0%; Pred. No. 3e-49;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGTGACCATGAAGGCTGCTGCTTCCCTGTTGATGCGAGGCTTGGCCCTGCAGCCAG 60
Db 50 CAGTGACCATGAAGGCTGCTGCTTCCCTGTTGATGCGAGGCTTGGCCCTGCAGCCAG 109
Qy 61 GCAGTGCCCTGCTGTGCTACTCTCTGCAAGCCGAGGTGAGCAACGAGGACTGCTGCAGG 120
Db 110 GCAGTGCCCTGCTGTGCTACTCTCTGCAAGCCGAGGTGAGCAACGAGGACTGCTGCAGG 169
Qy 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 180
Db 170 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGCGGCATCCGCGCAGTTGGCC 229
Qy 181 TCCTGACCGTCATCAGCAAGGCTGCAGTTGAACTGCGTGGATGACTCAGAGGACTACT 240
Db 230 TCCTGACCGTCATCAGCAAGGCTGCAGTTGAACTGCGTGGATGACTCAGAGGACTACT 289
Qy 241 ACCTGGGCAAGAAGAACATCACGTGCTGTGACACCGACT 279
Db 290 ACCTGGGCAAGAAGAACATCACGTGCTGTGACACCGACT 328

RESULT 5
CB147558
LOCUS
CB147558 550 bp mRNA linear EST 29-JAN-2003

```

DEFINITION K-EST0203584 L11SNU354s1 Homo sapiens cDNA clone L11SNU354s1-29-C07
 5', mRNA sequence.
 ACCESSION CB147558
 VERSION CB147558.1 GI:28129015
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 550)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 29 row: C column: 07
 High quality sequence stop: 550.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L11SNU354s1-29-C07"
 /sex="M"
 /tissue_type="liver"
 /cell_type="Polygonal"
 /cell_lines="SNU-354"
 /lab_host="Top10P"
 /clone_lib="L11SNU354s1"
 /note="Organ: Liver; Vector: PCNS-D2; Site 1: EcoRI;
 Site 2: NciI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 50nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10P, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library. After analyzing and
 sequencing about 2,000 - 3,000 colonies in original cDNA
 library, the abundant cDNAs were selected and amplified by
 PCR reaction using vector region primer including T7
 promoter as 5' primer and N(dT)14 as 3' primer. The PCR
 products were used as template for synthesis of
 biotinylated single stranded RNA by in vitro transcription
 reaction. The synthesized RNA probes were hybridized with
 antisense single stranded cDNAs prepared from original
 library and incubated with avidin-gel. After removing
 DNA-RNA hybrids by centrifuge, the subtracted cDNA
 libraries were constructed by transfection of the
 remaining DNA into competent cells E. coli Top10P, with
 electroporation method."

FEATURES
 source
 1..827
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5428261"
 /tissue_type="astrocytoma grade IV, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 398"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 279; DB 14; Length 827;
 Best Local Similarity 100.0%; Pred. No. 3.6e-49;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGTGACCATGAAGCGTGTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAG 60
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 DB 8 CAGTGACCATGAAGCGTGTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAG 67

Db 10 CAGTGACCATGAAGCGTGTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAG 69
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 Db 70 GCACCTGCCCTGCTGTGCTACTCTCTGAAAAGCCAGTGAGCAACGAGGACTGCCTGCAGG 129
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 QY 181 TCTGTACCGTCAATCAAGAAAGCTGCAGCTTGAACCTGCTGTGATGACTCACAGGACTACT 240
 |||||
 Db 190 TCTGTACCGTCAATCAAGAAAGCTGCAGCTTGAACCTGCTGTGATGACTCACAGGACTACT 249
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 QY 241 ACCTGGGCAAGAAACATCATCTGCTGTGACACCGACT 279
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 Db 250 ACCTGGGCAAGAAACATCATCTGCTGTGACACCGACT 288
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RESULT 6
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 LOCUS G03646652F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5428261 5',
 mRNA sequence.
 DEFINITION BM018750
 ACCESSION BM018750.1 GI:16533104
 VERSION EST.
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 827)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: LLCW1895 row: g column: 14
 High quality sequence stop: 810.
 Location/Qualifiers
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 /tissue_type="astrocytoma grade IV, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 398"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

FEATURES
 source
 1..827
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5428261"
 /tissue_type="astrocytoma grade IV, cell line"
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 /clone_lib="NIH MGC 398"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 279; DB 12; Length 827;
 Best Local Similarity 100.0%; Pred. No. 3.6e-49;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGTGACCATGAAGCGTGTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAG 60
 |||||
 DB 8 CAGTGACCATGAAGCGTGTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAG 67

Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGCTGCTTGCCTGCTGTGATGTCAGGCTTGGCCCTGCAGCCAG 60
 Db 8 CAGTGACCATGAAGGCTGCTGCTTGCCTGCTGTGATGTCAGGCTTGGCCCTGCAGCCAG 67
 QY 61 GCACTGCCCTGCTGCTGCTACTCTCTGCAAAAGCCAGCTGAGCAACGAGGACTGCTGCAGG 120
 Db 68 GCACTGCCCTGCTGCTGCTACTCTCTGCAAAAGCCAGCTGAGCAACGAGGACTGCTGCAGG 127
 QY 121 TCGAGACTGCACCCAGCTGGGGAGAGTGTGTCGACCCGCGCATCCCGCAGTTGGCC 180
 Db 128 TCGAGAACTGCACCCAGCTGGGGAGAGTGTGTCGACCCGCGCATCCCGCAGTTGGCC 187
 QY 181 TCCTGACCGTCAATCAGCAAAAGGCTGAGCTTGAATCTGCGTGGATGACTCACAGGACTACT 240
 Db 188 TCCTGACCGTCAATCAGCAAAAGGCTGAGCTTGAATCTGCGTGGATGACTCACAGGACTACT 247
 QY 241 ACCTGGGCAAGAAAGACATCACCTGCTGTGACACCGACT 279
 Db 248 ACCTGGGCAAGAAAGACATCACCTGCTGTGACACCGACT 286

RESULT 9
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 LOCUS
 DEFINITION
 AGENCOURT_13622529 NIH_MGC_148 Homo sapiens cDNA clone
 IMAGE:30337181 5', mRNA sequence.
 CB996183
 VERSION
 CB996183.1 GI:30290703
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 820)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM361 row: n column: 06
 High quality sequence stop: 597.

FEATURES
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 1..820
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30337181"
 /tissue_type="pre-eclampsia placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_148"
 /note="Organ: placenta; Vector: pBluescriptR; Site 1:
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 directionally cloned using primer
 5'-TTTTTTTTTTTTTTTTV-3', size-selected for average insert
 size 2.3 kb and normalized to ROT 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NHGRI, NHGRI,
 National Institutes of Health). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 99.4%; Score 277.4; DB 14; Length 820;

Best Local Similarity 99.6%; Pred. No. 7.8e-49;
 Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGCTGCTTGCCTGCTGTGATGTCAGGCTTGGCCCTGCAGCCAG 60
 Db 37 CAGTGACCATGAAGGCTGCTGCTTGCCTGCTGTGATGTCAGGCTTGGCCCTGCAGCCAG 96
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 Db 97 GCACTGCCCTGCTGCTGCTACTCTCTGCAAAAGCCAGCTGAGCAACGAGGACTGCTGCAGG 156
 QY 121 TCGAGAACTGCACCCAGCTGGGGAGAGTGTGTCGACCCGCGCATCCCGCAGTTGGCC 180
 Db 157 TCGAGAACTGCACCCAGCTGGGGAGAGTGTGTCGACCCGCGCATCCCGCAGTTGGCC 216
 QY 181 TCCTGACCGTCAATCAGCAAAAGGCTGAGCTTGAATCTGCGTGGATGACTCACAGGACTACT 240
 Db 217 TCCTGACCGTCAATCAGCAAAAGGCTGAGCTTGAATCTGCGTGGATGACTCACAGGACTACT 276
 QY 241 ACCTGGGCAAGAAAGACATCACCTGCTGTGACACCGACT 279
 Db 277 ACCTGGGCAAGAAAGACATCACCTGCTGTGACACCGACT 315

RESULT 10
 CB997275
 LOCUS
 DEFINITION
 AGENCOURT_13643348 NIH_MGC_148 Homo sapiens cDNA clone
 IMAGE:30336859 5', mRNA sequence.
 CB997275
 VERSION
 CB997275.1 GI:30291795
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 843)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM360 row: p column: 20
 High quality sequence stop: 612.

FEATURES
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 /mol_type="mRNA"
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 /clone="IMAGE:30336859"
 /tissue_type="pre-eclampsia placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_148"
 /note="Organ: placenta; Vector: pBluescriptR; Site 1:
 all-XhoI; Site 2: BamH; Library is oligo-dT primed and
 directionally cloned using primer
 5'-TTTTTTTTTTTTTTTTV-3', size-selected for average insert
 size 2.3 kb and normalized to ROT 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NHGRI, NHGRI,
 National Institutes of Health). Note: this is a NIH_MGC
 Library."

ORIGIN

3

Query Match 99.4%; Score 277.4; DB 14; Length 843;
 Best Local Similarity 99.6%; Pred. No. 7.9e-49;
 Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTTGCCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 60
 DB CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 135

QY 61 GCATGCGCTCTGCTGCTACTTCCGAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 120
 DB GCATGCGCTCTGCTGCTACTTCCGAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 195

QY 121 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGGCC 180
 DB TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGGCC 255

QY 181 TCCTGACCGTCATCAGCAAGGCTGCGAGCTTGAAGTGCCTGGATGACTCACAGGACTACT 240
 DB TCCTGACCGTCATCAGCAAGGCTGCGAGCTTGAAGTGCCTGGATGACTCACAGGACTACT 315

QY 241 ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGGACT 279
 DB ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGGACT 354

RESULT 11
 LOCUS CB993163 851 bp mRNA linear EST 01-MAY-2003
 DEFINITION AGENCOURT 13628816 NIH MGC 148 Homo sapiens cDNA clone
 IMAGE:30338013 5', mRNA sequence.

ACCESSION CB993163
 VERSION CB993163.1 GI:30287683
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 851)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Dr. Stefan Hanson
 Email: cgapbs-r@mail.nih.gov
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM363 row: p column: 22
 High quality sequence stop: 558.
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 /tissue_type="pre-eclamptic placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 148"
 /note="Organ: Placenta; Vector: pBluescriptR; Site_1:
 all-XhoI; Site_2: BamHI; Library is oligo-dr primed and
 directionally cloned using primer
 5'-TTTTTTTTTTTTTTT-3', size-selected for average insert
 size 2.3 kb and normalized to ROT 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NHGRI) and
 National Institutes of Health". Note: this is a NIH MGC
 Library."

FEATURES

Source
 1..851
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30338013"
 /tissue_type="pre-eclamptic placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 148"
 /note="Organ: Placenta; Vector: pBluescriptR; Site_1:
 all-XhoI; Site_2: BamHI; Library is oligo-dr primed and
 directionally cloned using primer
 5'-TTTTTTTTTTTTTTT-3', size-selected for average insert
 size 2.3 kb and normalized to ROT 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NHGRI) and
 National Institutes of Health". Note: this is a NIH MGC
 Library."

ORIGIN

Query Match

99.3%; Score 277; DB 12; Length 682;

Query Match 99.4%; Score 277.4; DB 14; Length 851;
 Best Local Similarity 99.6%; Pred. No. 7.9e-49;
 Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGTGACCATGAAGGCTGTGCTTGCCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 60
 DB CAGTGACCATGAAGGCTGTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAG 135

QY 61 GCATGCGCTCTGCTGCTACTTCCGAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 120
 DB GCATGCGCTCTGCTGCTACTTCCGAAAGCCAGGTGAGCAACGAGGACTGCTGCAGG 195

QY 121 TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGGCC 180
 DB TGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGGCC 255

QY 181 TCCTGACCGTCATCAGCAAGGCTGCGAGCTTGAAGTGCCTGGATGACTCACAGGACTACT 240
 DB TCCTGACCGTCATCAGCAAGGCTGCGAGCTTGAAGTGCCTGGATGACTCACAGGACTACT 315

QY 241 ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGGACT 279
 DB ACGTGGGCAAGAAGAACATCAGCTGCTGTGACACCGGACT 354

RESULT 12
 LOCUS BM042219 682 bp mRNA linear EST 07-NOV-2001
 DEFINITION 603616172F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5557096 5',
 mRNA sequence.

ACCESSION BM042219
 VERSION BM042219.1 GI:16771486
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 682)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTp
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2021 row: o column: 17
 High quality sequence stop: 678.
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 1..682
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGCAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

Source
 1..682
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5557096"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGCAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match

99.3%; Score 277; DB 12; Length 682;

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Best Local Similarity 100.0%; Pred. No. 8.8e-49;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAGGC 62
Db 2 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAGGC 61
QY 63 ACTGCCCTGTGCTGCTTACTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 122
Db 62 ACTGCCCTGTGCTGCTTACTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 121
QY 123 GAGAACTGCACCCAGCTGGGGAGCAGTCTGGACCGCGCATCGGCGAGTTGGCCCTC 182
Db 122 GAGAACTGCACCCAGCTGGGGAGCAGTCTGGACCGCGCATCGGCGAGTTGGCCCTC 181
QY 183 CTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACTAC 242
Db 182 CTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACTAC 241
QY 243 GTGGGCAAGAGAACATCAGCTGCTGTGACACCGACT 279
Db 242 GTGGGCAAGAGAACATCAGCTGCTGTGACACCGACT 278

RESULT 14
BG761095 60217425F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4840974 5',
LOCUS mRNA sequence.
DEFINITION 692 bp mRNA linear EST 15-MAY-2001
ACCESSION BG761095
VERSION 1 (bases 1 to 692)
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/BTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1673 row: a column: 07
High quality sequence stop: 690.
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1. 692
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/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

FEATURES
source
1. 692
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4840974"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 99.3%; Score 277; DB 12; Length 692;
Best Local Similarity 100.0%; Pred. No. 8.9e-49;

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Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAGGC 62
Db 2 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGCGAGGCTTGGCCCTGCAGCCAGGC 61
QY 63 ACTGCCCTGTGCTGCTTACTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 122
Db 62 ACTGCCCTGTGCTGCTTACTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 121
QY 123 GAGAACTGCACCCAGCTGGGGAGCAGTCTGGACCGCGCATCGGCGAGTTGGCCCTC 182
Db 122 GAGAACTGCACCCAGCTGGGGAGCAGTCTGGACCGCGCATCGGCGAGTTGGCCCTC 181
QY 183 CTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACTAC 242
Db 182 CTGACCGTCATCAGCAAGGCTGCAGCTTGAACCTGGTGGATGACTCAGGACTACTAC 241
QY 243 GTGGGCAAGAGAACATCAGCTGCTGTGACACCGACT 279
Db 242 GTGGGCAAGAGAACATCAGCTGCTGTGACACCGACT 278

RESULT 14
BG023582 standard; mRNA; HTC; 1024 BP.
ID BC023582
XX AC BC023582;
XX SV BC023582.1
XX DT 01-NOV-2002 (Rel. 73, Created)
XX DT 05-MAR-2003 (Rel. 75, Last updated, Version 3)
XX DE Homo sapiens, Similar to prostate stem cell antigen, clone IMAGE:4840974,
XX DE mRNA.
XX KW HTC.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX NIH-MGC Project URL: http://mgc.nci.nih.gov
XX 1-1024
XX Strausberg R.;
XX Submitted (05-FEB-2002) to the EMBL/GenBank/DBJ databases.
XX National Institutes of Health, Mammalian Gene Collection (MGC), Cancer
XX Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03,
XX Bethesda, MD 20892-2590, USA
XX RZPD; IRALp962M1933.
XX Contact: MGC help desk
XX Email: cgapbs-remail.nih.gov
XX Tissue Procurement: ATCC/DCTD/BTP
XX cDNA Library Preparation: Rubin Laboratory
XX cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
XX DNA Sequencing by: National Institutes of Health Intramural
XX Gaithersburg, Maryland;
XX Web site: http://www.nisc.nih.gov/
XX Contact: nisc.mgc@nih.gov
XX Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
XX Blakesley, R.W., Boufard, G.G., Breen, K., Brinkley, C., Brooks, S.,
XX Dietrich, N.B., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
XX Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
XX Maduro, C.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
XX McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
XX Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
XX Young, A., Zhang, L.-H. and Green, E.D.

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CC Clone distribution: MGC clone distribution information can be found
 CC through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 CC Series: IBAL Plate: 33 Row: m Column: 19
 CC This clone was selected for full length sequencing because it
 CC passed the following selection criteria: matched mRNA gi: 5031994
 CC This clone has the following problem: retained intron.

XX
 FH Key Location/Qualifiers
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 FT /note="vector: pOTB7"
 FT /organism="Homo sapiens"
 FT /clone="IMAGE:4840974"
 FT /tissue type="Skin, melanotic melanoma, high MDR."
 FT /clone_lib="NIH MGC 49"
 FT /lab_host="DH10B-R"
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 QY 3 GTGACCATGAAGGCTGCTGCTTGGCCCTGTGATGCGAGGCTTGGCCCTGCAGCCAGGC 62
 DB 10 GTGACCATGAAGGCTGCTGCTTGGCCCTGTGATGCGAGGCTTGGCCCTGCAGCCAGGC 69
 QY 63 ACTGCCCTGTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGGTTG 122
 DB 70 ACTGCCCTGTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGGTTG 129
 QY 123 GAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGGCACTCCGCGACTTGGCCCTC 182
 DB 130 GAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGGCACTCCGCGACTTGGCCCTC 189
 QY 183 CTGACCGCTCATCAGCAAGGCTGAGCTTGAACCTGGCTGGATGACTCAGGACTACTAC 242
 DB 190 CTGACCGCTCATCAGCAAGGCTGAGCTTGAACCTGGCTGGATGACTCAGGACTACTAC 249
 QY 243 GTGGGCAAGAGACATCAGTGTGTGACACCGACT 279
 DB 250 GTGGGCAAGAGACATCAGTGTGTGACACCGACT 286

RESULT 15
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 DEFINITION K-EST0026004 S9SNU601 Homo sapiens CDNA clone S9SNU601-30-E01 5',
 mRNA sequence.
 ACCESSION BM750435
 VERSION BM750435.1 GI:19080053
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 315)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 30 row: E column: 01

High quality sequence stop: 315.
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 /cell_type="Epithelial"
 /cell_line="SNU-601"
 /lab_host="Top10P"
 /clone_lib="S9SNU601"
 /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
 Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including SfiI
 site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized with Superscript II using SfiI
 oligo-dT primer. After first strand synthesis, RNA was
 degraded by NaOH treatment and cDNA was amplified by PCR
 reaction. The PCR products were digested with SfiI and
 cloned into DraIII- digested pME18S-FL3 vector. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 99.9%; Score 275.8; DB 12; Length 315;
 Best Local Similarity 99.3%; Pred. No. 1.2e-48;
 Matches 277; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAGTGACCATGAAGGCTGCTGCTTGGCCCTGTGATGCGAGGCTTGGCCCTGCAGCCAG 60
 DB 8 CAGTGACCATGAAGGCTGCTGCTTGGCCCTGTGATGCGAGGCTTGGCCCTGCAGCCAG 67
 QY 61 GCACTGCCCTGCTGTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCCCTGCAG 120
 DB 68 GCACTGCCCTGCTGTGCTACTCTCTCAAAAGCCAGGTGAGCAACGAGGACTGCCCTGCAG 127
 QY 121 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGGCACTCCGCGAGTTGGCC 180
 DB 128 TGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGGCACTCCGCGAGTTGGCC 187
 QY 181 TCCTGACCGTCAATCAGCAAAAGGCTGCAGCTTGAACCTGGCTGGATGACTCAGAGGACTACT 240
 DB 188 TCCTGACCGTCAATCAGCAAAAGGCTGCAGCTTGAACCTGGCTGGATGACTCAGAGGACTACT 247
 QY 241 ACGTGGGCAGAGAACATCAGCTGTGTGACACCGACT 279
 DB 248 ACGTGGGCAGAGAACATCAGCTGTGTGACACCGACT 286

Search completed: September 18, 2004, 19:14:22
 Job time : 1276.84 secs

Blank Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:35:58 ; Search time 1036.55 Seconds
(without alignments)
8655.682 Million cell updates/sec

Title: US-09-079-874-4
Perfect score: 207
Sequence: 1 GTGACCATGAAGGCTGTGCT.....TCATCAGCAAGGCTGCAGC 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
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27: em_sts.*
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30: em_htg_hum.*
31: em_htg_inv.*
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33: em_htg_mus.*
34: em_htg_pln.*
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37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	207	100.0	288	6	AR026990	Sequence
2	207	100.0	494	6	AR026974	Sequence
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4	207	100.0	990	6	AX014204	Sequence
5	207	100.0	990	6	BD205072	Human nuc
6	207	100.0	990	9	AF043498	Homo sapi
7	207	100.0	998	6	AR162849	Sequence
8	207	100.0	998	6	AR302232	Sequence
9	207	100.0	998	6	AX080304	Sequence
10	207	100.0	998	6	BD193367	Prostate
11	207	100.0	1015	9	BC023582	Homo sapi
12	205.4	99.2	979	6	BD076397	Human pro
13	205.4	99.2	998	6	BD264314	PSCA: pro
14	204.2	98.6	373	6	AX884747	Sequence
15	204.2	98.6	373	6	BD024357	Sequence
16	204.2	98.6	373	6	BD076969	5' EST of
17	201	97.1	372	6	AX155553	Sequence
18	199.4	96.3	369	6	BD076387	Human pro
19	195.8	94.6	232	6	AR026992	Sequence
20	190	91.8	960	6	AR410610	Sequence
21	190	91.8	960	6	AX201328	Sequence
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24	190	91.8	960	6	BD172241	Secreted
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38	112.4	54.3	157839	2	AC015718	Homo sapi
39	107.4	51.9	864	10	AF319173	Mus muscu
40	103.4	50.0	441	6	AR162850	Sequence
41	103.4	50.0	441	6	BD264315	PSCA: pro
42	103.4	50.0	441	6	AX302233	Sequence
43	103.4	50.0	441	6	AX080306	Sequence
44	103.4	50.0	441	6	BD193368	Prostate
45	58.8	28.4	190653	10	AC118022	Mus muscu

ALIGNMENTS

RESULT 1
AR026990
LOCUS: AR026990
DEFINITION: Sequence 23 from patent US 5856136.
ACCESSION: AR026990
VERSION: AR026990.1 GI:5937830
KEYWORDS: Unknown.
SOURCE: Unknown.
ORGANISM: Unclassified.
REFERENCE: 1 (bases 1 to 288)
AUTHORS: Au-Young, J.
TITLE: Human stem cell antigens
JOURNAL: Patent: US 5856136-A 23 05-JAN-1999;
FEATURES: Location/Qualifiers
linear DNA 288 bp PAT 29-SEP-1999

Pred. No. is the number of results predicted by chance to have a

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source      1..288
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Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTATGGCAGGCTTGGCCCTGCAGCCAGGC 60
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QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGCTGCAGGTG 120

QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCGGCGAGTTGGCCTC 180
DB 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCGGCGAGTTGGCCTC 180

QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207

RESULT 2
AR026974
LOCUS      494 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5856136.
ACCESSION AR026974
VERSION   AR026974.1 GI:5937814
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 494)
AUTHORS   Au-Young, J.
TITLE     Human stem cell antigens
JOURNAL   Patent: US 5856136-A 4 05-JAN-1999;
FEATURES
            Location/Qualifiers
            source      1..494
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                        /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 207; DB 6; Length 494;
Best Local Similarity 100.0%; Pred. No. 2.9e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 1 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTATGGCAGGCTTGGCCCTGCAGCCAGGC 60

QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGCTGCAGGTG 120

QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCGGCGAGTTGGCCTC 180
DB 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCGGCGAGTTGGCCTC 180

QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207

RESULT 3
HSA297436
LOCUS      946 bp      mRNA      linear      PRI 13-OCT-2000
DEFINITION Homo sapiens mRNA for prostate stem cell antigen (PSCA gene).
ACCESSION AJ297436
VERSION   AJ297436.1 GI:9367211

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KEYWORDS      prostate stem cell antigen; PSCA gene.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS       Bahrenberg, G., Bräuers, A., Joost, H.G. and Jakse, G.
TITLE         Reduced expression of PSCA, a member of the LY-6 family of cell
              surface antigens, in bladder, esophagus, and stomach tumors
              Biochem. Biophys. Res. Commun. 275 (3), 783-788 (2000)
              20431743
              PubMed 10973799
REFERENCE 2 (bases 1 to 946)
AUTHORS       Bahrenberg, G.
TITLE         Direct Submission
              Submitted (12-JUL-2000) Bahrenberg G., Institut fuer Pharmakologie
              und Toxikologie, RWTH Aachen, Wendlingweg2, Aachen, NRW, 52057,
              GERMANY
              Location/Qualifiers
              source      1..946
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /sex="female"
                        /tissue_type="urothelium"
                        /country="Germany"
              gene        1..946
                        /gene="PSCA"
              CDS         20..391
                        /gene="PSCA"
                        /function="unknown"
                        /note="GPI-anchored cell surface protein"
                        /codon_start=1
                        /product="prostate stem cell antigen"
                        /protein_id="CA97347.1"
                        /db_xref="GI:9367212"
                        /db_xref="GOA:O43653"
                        /db_xref="SWISS-PROT:O43653"
                        /translation="MKAVLLALLMAGLALPGTALLCYSCRAQVSNEDCLOVENTQQL
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Query Match      100.0%; Score 207; DB 9; Length 946;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 14 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTATGGCAGGCTTGGCCCTGCAGCCAGGC 73

QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 74 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGGACTGCTGCAGGTG 133

QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCGGCGAGTTGGCCTC 180
DB 134 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCGGCGAGTTGGCCTC 193

QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 194 CTGACCGTTCATCAGCAAAAGGCTGCAGC 220

RESULT 4
AX014204
LOCUS      990 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 108 from Patent WO9954447.
ACCESSION AX014204
VERSION   AX014204.1 GI:10040611
KEYWORDS

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmänn,B., Rosenthal,A. and
Pillarsky,C.
TITLE Human nucleic acid sequences of bladder tumour tissue
JOURNAL Patent: WO 9954447-A 198 28-OCT-1999;
BERND (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
FEATURES
source
1 . . 990
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 207; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
Db 12 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTGCTGTCTACTCTCGAAAGCCAGGCTGAGCAAGGAGCTGCCTGCAGGTG 120
Db 72 ACTGCCCTGCTGTCTACTCTCGAAAGCCAGGCTGAGCAAGGAGCTGCCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTC 180
Db 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTC 191
QY 181 CTGACCGTCTACGAAAGGCTGCAGC 207
Db 192 CTGACCGTCTACGAAAGGCTGCAGC 218
RESULT 5
BD205072 990 bp DNA linear PAT 17-JUL-2003
LOCUS Human nucleic acid sequence originating in cystic cancer tissue.
DEFINITION BD205072
ACCESSION BD205072.1 GI:33014842
VERSION JP 2002512023-A/26.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 990)
AUTHORS Specht,T., Hinzmänn,B., Schmitt,A., Pillarsky,C., Dahl,E. and
Rosenthal,A.
TITLE Human nucleic acid sequence originating in cystic cancer tissue
JOURNAL Patent: JP 2002512023-A 26 23-APR-2002;
METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
COMMENT OS Homo sapiens (human)
PN JP 2002512023-A/26
PD 23-APR-2002
PF 15-APR-1999 JP 2000544779
PR 21-APR-1998 DE 198 18 619.3
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
PI EDGAR DAHL,
PI ANDRE ROSENTHAL
PC C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P13/10,
PC A61P35/00,
PC C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12P21/08,C12Q1/68, PC
C12N15/00,
PC A61K37/02,C12N5/00
CC Human nucleic acid sequence originating in cystic cancer CC
tissue
PH Key Location/Qualifiers

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/organism="Homo sapiens (human)"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Query Match 100.0%; Score 207; DB 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
Db 12 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTGCTGTCTACTCTCGAAAGCCAGGCTGAGCAAGGAGCTGCCTGCAGGTG 120
Db 72 ACTGCCCTGCTGTCTACTCTCGAAAGCCAGGCTGAGCAAGGAGCTGCCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTC 180
Db 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGCATCCGCGCAGTTGGCCTC 191
QY 181 CTGACCGTCTACGAAAGGCTGCAGC 207
Db 192 CTGACCGTCTACGAAAGGCTGCAGC 218
RESULT 6
AF043498 990 bp mRNA linear PRI 24-FEB-1998
LOCUS Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds.
DEFINITION AF043498
ACCESSION AF043498
VERSION AF043498.1 GI:2909843
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 990)
AUTHORS Reiter,R.E., Gu,Z., Watabe,T., Thomas,G., King,S., Davis,B.,
Wahl,M., Nisitani,S., Yamashiro,J., Le Beau,M.M., Losa,M. and
Witte,O.N.
TITLE Prostate stem cell antigen: a cell surface marker overexpressed in
prostate cancer
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (4), 1735-1740 (1998)
MEDLINE 98132661
PUBMED 9465086
REFERENCE 2 (bases 1 to 990)
AUTHORS Reiter,R.E.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1998) Urology, UCLA, 66-134 CHS 10833 Le Conte
Ave., Los Angeles, CA 90095, USA
FEATURES
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/mol_type="mRNA"
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18 . . 389
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/codon_start=1
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/protein_id="AAC39607.1"
/db_xref="GI:2909844"
/translation="MKAVLLALLMAGLQFGTALLCYSCAKQVSNEDCLQVENCQL"

GEQWTRARIRAVGLLTIVISKGSLNCVDDSDQYVYVKNIITCCDTDLNAGSAHALQP
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ORIGIN

Query Match 100.0%; Score 207; DB 9; Length 990;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 12 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 72 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 180
DB 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 191
QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 192 CTGACCGTTCATCAGCAAAAGGCTGCAGC 218

RESULT 7
AR162849
LOCUS AR162849 998 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6258939.
ACCESSION AR162849
VERSION AR162849.1 GI:16230194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 998)
AUTHORS Reiter,R.E. and Witte,O.N.
TITLE PSCA antibodies and hybridomas producing them
JOURNAL Patent: US 6258939-A 1 10-JUL-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 207; DB 6; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 12 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 72 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 180
DB 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 191
QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 192 CTGACCGTTCATCAGCAAAAGGCTGCAGC 218

RESULT 8
AR302232
LOCUS AR302232 998 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6541212.
ACCESSION AR302232
VERSION AR302232.1 GI:31690451
KEYWORDS

Unknown.
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 998)
AUTHORS Reiter,R.E. and Witte,O.N.
TITLE Methods for detecting prostate stem cell antigen protein
JOURNAL Patent: US 6541212-A 1 01-APR-2003;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 207; DB 6; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 12 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 72 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 180
DB 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 191
QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 192 CTGACCGTTCATCAGCAAAAGGCTGCAGC 218

RESULT 9
AX080304
LOCUS AX080304 998 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 1 from Patent WO0105427.
ACCESSION AX080304
VERSION AX080304.1 GI:13159773
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
UNCLASSIFIED.

REFERENCE 1
AUTHORS Reiter,R., Witte,O., Saffran,D.C. and Jakobovits,A.
TITLE Prostate stem cell antigen and uses thereof
JOURNAL Patent: WO 0105427-A 1 25-JAN-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) ; Urogenesys, Inc. (US)

FEATURES Location/Qualifiers
source
1..998
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 207; DB 6; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 12 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 72 ACTGCCCTCTGCTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 180
DB 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCGCATCCGGCGCAGTTGGCCTC 191

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ORIGIN

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Query Match      100.0%; Score 207; DB 9; Length 1015;
Best Local Similarity 100.0%; Pred. No. 2.5e-33;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
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QY 61 ACTGCCCTGCTGTCTACTCTCTGCAAGCCAGGAGGAGCAAGGAGCTGCTGCAGGTG 120
Db 61 ACTGCCCTGCTGTCTACTCTCTGCAAGCCAGGAGGAGCAAGGAGCTGCTGCAGGTG 120
QY 121 GAGAACTGCACCCAGCTGGGGAGGAGCTGCTGGACCGCGCGCATCCGCGAGTTGGCCTC 180
Db 121 GAGAACTGCACCCAGCTGGGGAGGAGCTGCTGGACCGCGCGCATCCGCGAGTTGGCCTC 180
QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
Db 181 CTGACCGTCATCAGCAAGGCTGCAGC 207

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RESULT 12
BD076397
LOCUS
DEFINITION
Human protein having transmembrane domain and DNA encoding the
same.
ACCESSION
BD076397
VERSION
JP 2001519154-A/11.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 979)
AUTHORS
Kato, S., Kimura, T., Sekine, S. and Kobayashi, M.
TITLE
Human protein having transmembrane domain and DNA encoding the same
Patent: JP 2001519154-A 11 23-OCT-2001.
JOURNAL
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
COMMENT
OS Homo sapiens (human)
PN JP 2001519154-A/11
PD 23-OCT-2001
PF 05-OCT-1998 JP 2000515001
PI SETSUKI KATO, TOMOKO KIMURA, SHINGO SEKINE, MIDORI KOBAYASHI PC
C12N15/09, C07K14/47, C12N15/10, C12N15/00, C12N15/00 CC Human protein
having transmembrane domain
and DNA encoding the
CC same
FT source
FT source
FT source

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FEATURES
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1..979
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match      99.2%; Score 205.4; DB 6; Length 998;
Best Local Similarity 99.5%; Pred. No. 5.5e-33;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
Db 12 GTGACCGTGAAGGCTGTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
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Query Match      99.2%; Score 205.4; DB 6; Length 979;
Best Local Similarity 99.5%; Pred. No. 5.5e-33;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
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QY 121 GAGAACTGCACCCAGCTGGGGAGGAGCTGCTGGACCGCGCGCATCCGCGAGTTGGCCTC 180
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QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
Db 190 CTGACCGTCATCAGCAAGGCTGCAGC 216

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RESULT 13
BD264314
LOCUS
DEFINITION
PSCA: prostate stem cell antigen and uses thereof.
ACCESSION
BD264314
VERSION
JP 2002531082-A/1.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 998)
AUTHORS
Reiter, R. and Witte, O.
TITLE
PSCA: prostate stem cell antigen and uses thereof
Patent: JP 2002531082-A 1 24-SEP-2002;
JOURNAL
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT
OS Homo sapiens (human)
PN JP 2002531082-A/1
PD 24-SEP-2002
PF 02-DEC-1999 JP 2000585383
PR 02-DEC-1998 US 09/203939, 17-FEB-1999 US 09/251835 PR
25-MAY-1999 US 09/318503
PI ROBERT REITER, OWEN WITTE
PC C12N15/09, A01K67/02, A61K35/76, A61K45/00, A61P15/00,
PC A61P35/00,
PC C07K14/47, C07K16/18, C12N5/10, C12N15/02, C12P21/00, C12Q1/02, PC
C12Q1/68,
PC GOIN33/53, GOIN33/53, GOIN33/566, GOIN33/574, GOIN33/58/CI2P21/08, PC
C12N15/00,
PC C12N15/00, C12N5/00
CC human PSCA (hPSCA)
FH Key
FT source
FT source

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FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
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Query Match      99.2%; Score 205.4; DB 6; Length 998;
Best Local Similarity 99.5%; Pred. No. 5.5e-33;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 72 ACTGCCCTGCTGTGCTACTCTCGAAAGCCAGGTGAGCAACGAGACTGCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGAGAGTGTGAGACCGCGGCATCCGGCAGTTGGCCTC 180
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QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
Db 192 CTGACCGTTCATCAGCAAAAGGCTGCAGC 218

RESULT 14
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LOCUS AX884747 373 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 610 from Patent EP1033401.
ACCESSION AX884747
VERSION AX884747.1 GI:40040217
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 610 06-SEP-2000;
Genset (FR)

FEATURES
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Matches 203; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 163 ACTGCCCTGCTGTGCTACTCTCGAARGCCAGGTGAGCAACGAGACTGCTGCAGGTG 222
QY 121 GAGAACTGCACCCAGCTGGGGAGAGTGTGAGACCGCGGCATCCGGCAGTTGGCCTC 180
Db 223 GAGAACTGCACCCAGCTGGGGAGAGTGTGAGACCGCGGCATCCGGCAGTTGGCCTC 282
QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
Db 283 CTGACCGTTCATCAGCAAAAGGCTGCAGC 309

RESULT 15
BD024357
LOCUS BD024357 373 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD024357
VERSION BD024357.1 GI:22565580
KEYWORDS JP 2001269182-A/603.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 373)
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 603 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/603
PD 02-OCT-2001
PR 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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CC score 7.5
CC seq AVLLALLMAGLAL/QP
FH Key Location/Qualifiers
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Best Local Similarity 98.1%; Pred. No. 1.2e-32;
Matches 203; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGCGCTGTGCTGTGCCCTGTGATGGCAGGCTTGCCCTGCAGCCAGGC 60
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QY 61 ACTGCCCTGCTGTGCTACTCTCGAAAGCCAGGTGAGCAACGAGACTGCTGCAGGTG 120
Db 163 ACTGCCCTGCTGTGCTACTCTCGAARGCCAGGTGAGCAACGAGACTGCTGCAGGTG 222
QY 121 GAGAACTGCACCCAGCTGGGGAGAGTGTGAGACCGCGGCATCCGGCAGTTGGCCTC 180
Db 223 GAGAACTGCACCCAGCTGGGGAGAGTGTGAGACCGCGGCATCCGGCAGTTGGCCTC 282
QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
Db 283 CTGACCGTTCATCAGCAAAAGGCTGCAGC 309

Search completed: September 18, 2004, 13:27:07
Job time : 1037.55 secs

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OM nucleic - nucleic search, using sw model
Run on: September 18, 2004, 04:33:41 ; Search time 135,318 Seconds
(without alignments)
6498.387 Million cell updates/sec

Title: US-09-079-874-4
Perfect score: 207
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:*
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5: Geneseqn2001bs:*
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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	207	100.0	207	2	Aav80389 Nucleotid
2	207	100.0	207	2	Aav68606 Human P81
3	207	100.0	279	2	Aav80388 Nucleotid
4	207	100.0	279	2	Aav68605 Human P81
5	207	100.0	288	2	Aav38061 Human ste
6	207	100.0	233	2	Aav80387 Nucleotid
7	207	100.0	233	2	Aav68604 Human P81
8	207	100.0	494	2	Aav38045 Human ste
9	207	100.0	972	2	Aav80396 Nucleotid
10	207	100.0	990	7	ACC51040 Human bla
11	207	100.0	990	7	ABQ3853 Human PSC
12	207	100.0	990	9	ADC09589 PSCA cDNA
13	207	100.0	998	4	ABK09980 Human pro
14	207	100.0	998	5	Aaf27971 Human pro
15	207	100.0	1023	2	Aav80397 Consensus
16	207	100.0	1023	2	Aav68613 Human P81
17	207	100.0	1023	2	Aav68614 Human P81
18	207	100.0	1028	9	Ades3926 Human pro
19	205.4	99.2	979	2	Aax36801 Human tra
20	205.4	99.2	998	2	Aav33691 Human pro
21	205.4	99.2	998	3	AAA48374 Human pro
22	204.2	98.6	373	2	AAX40622 Human sec
23	204.2	98.6	373	3	AAC00612 Human sec

24	201	97.1	372	4	AAD08171	Aad08171 Human pro
25	199.4	96.3	369	2	AAX36800	Aax36800 Human tra
26	198	95.7	290	2	AAV80386	Aav80386 Nucleotid
27	198	95.7	230	2	AAV86603	Aav68603 Human P81
28	195.8	94.6	232	2	AAV38063	Aav38063 Human ste
29	190	91.8	960	2	AAX52217	Aax52217 Protein P
30	190	91.8	960	3	ADC78337	Adc78337 Human PRO
31	190	91.8	960	4	AAF72375	Aaf72375 Human PRO
32	190	91.8	960	6	ABK40257	Abk40257 cDNA enco
33	190	91.8	960	7	ACA58909	Aca58909 Human PRO
34	190	91.8	960	7	ACA58306	Aca58306 cDNA enco
35	190	91.8	960	7	ACA60013	Aca60013 Human CDN
36	190	91.8	960	7	ACD07413	Acc07413 Novel hum
37	190	91.8	960	7	ABX71461	Abx71461 Human CDN
38	190	91.8	960	7	ACH06793	Ach06793 Human sec
39	190	91.8	960	7	ABX96030	Abx96030 Human sec
40	190	91.8	960	7	ACA05351	Aca05351 cDNA enco
41	190	91.8	960	7	ACD20018	Acd20018 Human sec
42	190	91.8	960	7	ACA54821	Aca54821 Novel hum
43	190	91.8	960	8	ACD19656	Acd19656 Human sec
44	190	91.8	960	8	ADB29222	Adb29222 Human sec
45	190	91.8	960	8	ADA18078	Ada18078 Human sec

ALIGNMENTS

RESULT 1
AAV80389
ID AAV80389 standard; DNA; 207 BP.
XX
AC AAV80389;
XX
DT 23-FEB-1999 (first entry)
XX
DE Nucleotide sequence of UTI16 gene-specific clone 1543671.
XX
KW UTI16; urinary tract; epitope; antigen; detection; diagnosing;
KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
KW metastasis; ss.
XX
OS Homo sapiens.
XX
FN WO9851824-A1.
XX
PD 19-NOV-1998.
XX
PF 15-MAY-1998; 98WO-US009972.
XX
PR 15-MAY-1997; 97US-00856652.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
Stroupe SD;
XX
XX WPI; 1999-045237/04.
XX
PT New method for detecting diseases of the urinary tract - comprises use of
a UTI16 polynucleotide, protein or antibodies, used for preventing and
treating urinary tract infections and cancer.
XX
PS Claim 1; Fig 1A-C; 113pp; English.
XX
CC Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
sequences of the UTI16 gene-specific clones derived from urinary tract
tissue. The invention relates to a method of detecting the presence of a
target UTI16 polynucleotide in a test sample using these UTI16-specific
sequences. Host cells transfected with an expression vector containing
the UTI16 gene can be used to produce a UTI16 polypeptide recombinantly.
CC This polypeptide has at least one UTI16 epitope which can be used in a
method for detecting UTI16 antigen in a test sample. The polynucleotides

CC	and polypeptides are useful for detecting, diagnosing, monitoring,	CC	PS116 polypeptides or PS116 amplicons are used to detect prostate
CC	staging, prognosticating, in vivo imaging, preventing, treating or	CC	disease. Antibodies (Abs) against PS116 are used in assay kits to detect
CC	determining the predisposition of a subject to diseases and conditions of	CC	PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
CC	the urinary tract, such as urinary tract cancer. Antibodies specifically	CC	solid phase. The polypeptides are used for detecting PS116-specific Abs
CC	binding to an epitope of UT116 antigen, and agonists are useful for	CC	in a sample, and for producing Abs after immunising a subject. Plasmids
CC	treating urinary tract diseases, tumours and metastases	CC	encoding PS116 epitopes can also be administered to a subject to obtain
XX		CC	Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
SQ	Sequence 207 BP; 37 A; 65 C; 68 G; 37 T; 0 U; 0 Other;	CC	staging, monitoring, prognosticating, in vivo imaging, preventing,
	Query Match 100.0%; Score 207; DB 2; Length 207;	CC	treating or determining the predisposition of a subject to diseases and
	Best Local Similarity 100.0%; Pred. No. 1.6e-40;	CC	conditions of the prostate, such as prostate cancer. The Abs and agonists
	Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	or inhibitors are useful for treating prostate diseases, tumours and
		CC	metastases
QY	1 GTGACCATGAAGCTGTGCTGCTTCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60	SQ	Sequence 207 BP; 37 A; 65 C; 68 G; 37 T; 0 U; 0 Other;
Db	1 GTGACCATGAAGCTGTGCTGCTTCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60		Query Match 100.0%; Score 207; DB 2; Length 207;
QY	61 ACTGCCCTGCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGACTGCTGCAGGTG 120		Best Local Similarity 100.0%; Pred. No. 1.6e-40;
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QY	181 CTGACCGTTCATCAGCAAGGCTGCAGC 207	QY	61 ACTGCCCTGCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGACTGCTGCAGGTG 120
Db	181 CTGACCGTTCATCAGCAAGGCTGCAGC 207	Db	61 ACTGCCCTGCTGTGCTACTCTCTGCAAGCCCAAGGTGAGCAACGAGACTGCTGCAGGTG 120
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ID	AAV68606 standard; cDNA; 207 BP.	RESULT 3	
AC	AAV68606;	AAV80388	
XX		ID	AAV80388 standard; DNA; 279 BP.
DT	16-MAR-1999 (first entry)	XX	XX
DE	Human PS116 EST clone 1543671.	AC	AAV80388;
XX		XX	XX
XX	Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;	DT	23-FEB-1999 (first entry)
KW	detection; therapy; prostate cancer; metastasis; ss.	XX	XX
OS	Homo sapiens.	DE	Nucleotide sequence of UT116 gene-specific clone 1891065.
XX		XX	UT116; urinary tract; epitope; antigen; detection; diagnosing;
PN	WO9851805-A1.	KW	monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
XX		KW	metastasis; ss.
PD	19-NOV-1998.	XX	XX
XX		OS	Homo sapiens.
XX	15-MAY-1998; 98WO-US010041.	XX	XX
XX		XX	WO9851824-A1.
XX	15-MAY-1997; 97US-00856653.	PN	19-NOV-1998.
XX		PD	15-MAY-1998; 98WO-US009972.
XX	(ABBO) ABBOTT LAB.	PF	15-MAY-1997; 97US-00856652.
PI	Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;	XX	XX
PI	Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;	XX	(ABBO) ABBOTT LAB.
PI	Russell JC, Stroupe SD;	XX	XX
XX		XX	Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
XX	WPI; 1999-045234/04.	XX	Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
XX		XX	Stroupe SD;
XX	New method for detecting diseases of the prostate - comprises use of a	DR	WPI; 1999-045237/04.
PT	PS116 polynucleotide, protein or antibodies, useful for preventing and	XX	XX
PT	treating prostate infections and cancer.	XX	New method for detecting diseases of the urinary tract - comprises use of
XX		XX	a UT116 polynucleotide, protein or antibodies, used for preventing and
XX	Claim 1; Page 92; 118pp; English.	XX	treating urinary tract infections and cancer.
XX		XX	XX
XX	This sequence represents an expressed sequence tag (EST) clone of the	PS	Claim 1; Fig 1A-C; 113pp; English.
CC	PS116 gene isolated from a human prostate tissue library. This sequence		
CC	can be used in the method of the invention for detecting a target PS116		
CC	polynucleotide (PN), that comprises: contacting a sample with at least 1		
CC	PS116-specific PN or complement; and detecting the target PS116 PN, where		
CC	the specific PN has at least 50% identity with this sequence. The PNs,		

XX Sequences AAV0386 to AAV0396 represent partially overlapping nucleotide
CC sequences of the Utl16 gene-specific clones derived from urinary tract
CC tissue. The invention relates to a method of detecting the presence of a
CC target Utl16 polynucleotide in a test sample using these Utl16-specific
CC sequences. Host cells transfected with an expression vector containing
CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
CC This polypeptide has at least one Utl16 epitope which can be used in a
CC method for detecting Utl16 antigen in a test sample. The polynucleotides
CC and polypeptides are useful for detecting, diagnosing, monitoring,
CC staging, prognosticating, in vivo imaging, preventing, treating or
CC determining the predisposition of a subject to diseases and conditions of
CC the urinary tract, such as urinary tract cancer. Antibodies specifically
CC binding to an epitope of Utl16 antigen, and agonists are useful for
CC treating urinary tract diseases, tumours and metastases
XX
SQ Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 207; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGSCAGGCTTGGCCCTGCAGCCAGGC 60
DB 3 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGSCAGGCTTGGCCCTGCAGCCAGGC 62
QY 61 ACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTGCAGGTG 120
DB 63 ACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTGCAGGTG 122
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DB 183 CTGACCGTTCATCAGCAAGGCTGCAGC 209

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AAV68605
ID AAV68605 standard; cDNA; 279 BP.

AC AAV68605;

DT 16-MAR-1999 (first entry)

DE Human PS116 EST clone 1891065.

XX Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
KW detection; therapy; prostate cancer; metastasis; ss.

XX Homo sapiens.

OS WO9851805-A1.

XX 19-NOV-1998.

PD 15-MAY-1998; 98WO-US010041.

XX 15-MAY-1997; 97US-00856653.

PA (ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;

DR WPI; 1999-045234/04.

XX New method for detecting diseases of the prostate - comprises use of a
PT PS116 polynucleotide, protein or antibodies, useful for preventing and
PT treating prostate infections and cancer.

XX Claim 1; Page 92; 119pp; English.

XX This sequence represents an expressed sequence tag (EST) clone of the
CC PS116 gene isolated from a human prostate tissue library. This sequence
CC can be used in the method of the invention for detecting a target PS116
CC polynucleotide (PN), that comprises: contacting a sample with at least 1
CC PS116-specific PN or complement; and detecting the target PS116 PN, where
CC the specific PN has at least 50% identity with this sequence. The PNs,
CC PS116 polypeptides or PS116 amplicons are used to detect prostate
CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
CC solid phase. The polypeptides are used for detecting PS116-specific Abs
CC in a sample, and for producing Abs after immunising a subject. Plasmids
CC encoding PS116 epitopes can also be administered to a subject to obtain
CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC treating or determining the predisposition of a subject to diseases and
CC conditions of the prostate, such as prostate cancer. The Abs and agonists
CC or inhibitors are useful for treating prostate diseases, tumours and
CC metastases
XX

SQ Sequence 279 BP; 58 A; 83 C; 87 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 207; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 1.6e-40;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGSCAGGCTTGGCCCTGCAGCCAGGC 60

DB 3 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGSCAGGCTTGGCCCTGCAGCCAGGC 62

QY 61 ACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTGCAGGTG 120

DB 63 ACTGCCCTGTGCTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTGCAGGTG 122

QY 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGSCCTC 180

DB 123 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGSCCTC 182

QY 181 CTGACCGTTCATCAGCAAGGCTGCAGC 207

DB 183 CTGACCGTTCATCAGCAAGGCTGCAGC 209

RESULT 5

AAV38061

ID AAV38061 standard; cDNA; 288 BP.

XX AAV38061;

AC AAV38061;

DT 14-SEP-1998 (first entry)

DE Human stem cell antigen 2 partial sequence from Incyte clone 1312529.

XX Human; stem cell antigen; SCNAH-1; SCNAH-2; THP-1; bladder tumour;
KW diagnosis; screening; sca-2; LY-6 family; leukaemia; cancer; ss.

XX Homo sapiens.

OS WO9800540-A1.

XX 08-JAN-1998.

XX 25-JUN-1997; 97WO-US010956.

XX 03-JUL-1996; 96US-00675508.

PA (INCYTE) INCYTE PHARM INC.

PI Au-Young J;

XX WPI; 1998-427478/36.

```
XX Human stem cell antigens, SCAH-1 and SCAH-2 - useful to, e.g. diagnose
PT and treat SCAH-1 or SCAH-2 related conditions such as tumours and screen
PT inhibitory compounds.
XX
XX Disclosure; Page 49; 66pp; English.
XX
XX The present sequence represents an Incyte clone used in the determination
CC of human stem cell antigen 2 (SCAH-2). SCAH proteins can be administered
CC therapeutically, e.g. to inhibit or reverse the development of tumours.
CC Antibodies to SCAH proteins can be used in diagnostic tests for
CC conditions associated with protein expression in biological samples, by
CC combining a sample with the antibody under conditions suitable for
CC antibody binding to the protein to form a complex, and detecting the
CC complex. Antibodies to SCAH-2 are especially useful in diagnostic tests
CC for conditions/diseases such as leukaemias or malignant local tumours
CC associated with SCAH-2 expression. SCAH-1 and SCAH-2 have homology to Sca
CC -2 and other stem cell antigens, and have characteristics of the LY-6
CC family of cysteine rich proteins. The functional similarities among LY-6
CC family proteins previously reported, and the expression of SCAH-1 and
CC SCAH-2 in tumours from several tissues (e.g. breast, lung, bladder)
CC indicated that SCAH proteins may be useful as anticancer agents; SCAH
CC antibodies, antagonists or inhibitors identified using the proteins could
CC also be useful in anticancer treatments and to intervene in alloresponses
CC associated with transplant rejection and autoimmune diseases e.g. lupus
CC nephritis. The nucleic acid sequences encoding SCAH proteins are also
CC useful therapeutically to treat, e.g. leukaemias and cancers of the
CC bladder or breast
XX
XX Sequence 288 BP; 60 A; 85 C; 90 G; 53 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 207; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 1 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
QY 61 ACTGCCCTGCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAGGACTGCTGCAGGTG 120
DB 61 ACTGCCCTGCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAGGACTGCTGCAGGTG 120
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DB 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGAGCCGCGCGCATCCGGCGAGTTGGCCTC 180
QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
RESULT 6
AAV80387
ID AAV80387 standard; DNA; 293 BP.
XX
XX AAV80387;
XX
XX 23-FEB-1999 (first entry)
XX
XX Nucleotide sequence of UT116 gene-specific clone 2804743.
XX
XX UT116; urinary tract; epitope; antigen; detection; diagnosing;
XX monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
XX metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO951824-A1.
XX
XX 19-NOV-1998.
XX
XX 15-MAY-1998; 98WO-US009972.
XX
XX PF
XX
XX PR 15-MAY-1997; 97US-00856652.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
PI Stroupe SD;
XX
XX WPI; 1999-045237/04.
XX
XX New method for detecting diseases of the urinary tract - comprises use of
PT a UT116 polynucleotide, protein or antibodies, used for preventing and
PT treating urinary tract infections and cancer.
XX
XX Claim 1; Fig 1A-C; 113pp; English.
XX
XX Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
CC sequences of the UT116 gene-specific clones derived from urinary tract
CC tissue. The invention relates to a method of detecting the presence of a
CC target UT116 polynucleotide in a test sample using these UT116-specific
CC sequences. Host cells transfected with an expression vector containing
CC the UT116 gene can be used to produce a UT116 polypeptide recombinantly.
CC This polypeptide has at least one UT116 epitope which can be used in a
CC method for detecting UT116 antigen in a test sample. The polynucleotides
CC and polypeptides are useful for detecting, diagnosing, monitoring,
CC staging, prognosticating, in vivo imaging, preventing, treating or
CC determining the predisposition of a subject to diseases and conditions of
CC the urinary tract, such as urinary tract cancer. Antibodies specifically
CC binding to an epitope of UT116 antigen, and agonists are useful for
CC treating urinary tract diseases, tumours and metastases
XX
XX Sequence 293 BP; 60 A; 92 C; 89 G; 52 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 207; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 27 GTGACCATGAAGGCTGTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 86
QY 61 ACTGCCCTGCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAGGACTGCTGCAGGTG 120
DB 87 ACTGCCCTGCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAGGACTGCTGCAGGTG 146
QY 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGAGCCGCGCGCATCCGGCGAGTTGGCCTC 180
DB 147 GAGAACTGCACCCAGCTGGGGAGCAGTGTGAGCCGCGCGCATCCGGCGAGTTGGCCTC 206
QY 181 CTGACCGTTCATCAGCAAAAGGCTGCAGC 207
DB 207 CTGACCGTTCATCAGCAAAAGGCTGCAGC 233
RESULT 7
AAV68604
ID AAV68604 standard; cDNA; 293 BP.
XX
XX AAV68604;
XX
XX 16-MAR-1999 (first entry)
XX
XX Human PS116 EST clone 2804743.
XX
XX Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
XX detection; therapy; prostate cancer; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO951805-A1.
XX
XX 19-NOV-1998.
XX
XX PD
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RESULT 9
 AAV80396
 ID AAV80396 standard; DNA; 972 BP.
 XX
 AC AAV80396;
 XX
 DT 23-FEB-1999 (first entry)
 XX
 DE Nucleotide sequence of UT116 gene-specific clone 1543671H.
 XX
 KW UT116; urinary tract; epitope; antigen; detection; diagnosing;
 KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
 KW metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..378
 FT /*tag= a
 FT /product= "UT116 polypeptide"
 XX
 PN WO9851824-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 15-MAY-1998; 98WO-US0009972.
 XX
 PR 15-MAY-1997; 97US-00856652.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
 PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
 PI Stroupe SD;
 XX
 DR WPI; 1999-045237/04.
 DR P-PSDB; AAN86024.
 XX
 PT New method for detecting diseases of the urinary tract - comprises use of
 PT a UT116 polynucleotide, protein or antibodies, used for preventing and
 PT treating urinary tract infections and cancer.
 XX
 PS Claim 1; Fig 1A-C; 113pp; English.
 XX
 CC Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide
 CC sequences of the UT116 gene-specific clones derived from urinary tract
 CC tissue. The invention relates to a method of detecting the presence of a
 CC target UT116 polynucleotide in a test sample using these UT116-specific
 CC sequences. Host cells transfected with an expression vector containing
 CC the UT116 gene can be used to produce a UT116 polypeptide recombinantly.
 CC This polypeptide has at least one UT116 epitope which can be used in a
 CC method for detecting UT116 antigen in a test sample. The polynucleotides
 CC and polypeptides are useful for detecting, diagnosing, monitoring,
 CC staging, prognosticating, in vivo imaging, preventing, treating or
 CC determining the predisposition of a subject to diseases and conditions of
 CC the urinary tract, such as urinary tract cancer. Antibodies specifically
 CC binding to an epitope of UT116 antigen, and agonists are useful for
 CC treating urinary tract diseases, tumours and metastases
 XX
 SQ Sequence 972 BP; 180 A; 330 C; 280 G; 182 T; 0 U; 0 Other;
 Query Match 100.0%; Score 207; DB 2; Length 972;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACCATGAAGGCTGTGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
 Db 1 GTGACCATGAAGGCTGTGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
 QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGCCGAGGTGAGCAACGAGACTGCTGCAGGTG 120

Db 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCCAAGCCGAGGTGAGCAACGAGACTGCTGCAGGTG 120
 QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCCCGCGCATCGCCGAGTTGCGCTC 180
 Db 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCCCGCGCATCGCCGAGTTGCGCTC 180
 QY 181 CTGACCGCTCATCAGCAAAAGGCTGCAGC 207
 Db 181 CTGACCGCTCATCAGCAAAAGGCTGCAGC 207
 RESULT 10
 ACC51040
 ID ACC51040 standard; cDNA; 990 BP.
 XX
 AC ACC51040;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human bladder cancer associated cDNA sequence SEQ ID NO:168.
 XX
 KW Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003003906-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 03-JUL-2002; 2002WO-US021338.
 XX
 PR 03-JUL-2001; 2001US-0302814P.
 PR 03-AUG-2001; 2001US-0310099P.
 PR 08-NOV-2001; 2001US-0343705P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Mack DH, Aziz N;
 XX
 DR WPI; 2003-201532/19.
 DR P-PSDB; ABR48224.
 XX
 PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 XX
 PS Claim 6; Page 288; 307pp; English.
 XX
 CC The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications
 XX
 SQ Sequence 990 BP; 193 A; 299 C; 285 G; 202 T; 0 U; 11 Other;
 Query Match 100.0%; Score 207; DB 7; Length 990;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACCATGAAGGCTGTGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60

Db 12 GTGACCATGAAGCTGTGCTGCTTGGCCCTGTGATGCGAGCTTGGCCCTGCAGCCAGCG 71
 QY 61 ACTGCCCTGCTGCTACTCTCTGAAAGCCAGCTGAGCAACAGAGACTGCTGCAGGTG 120
 Db 72 ACTGCCCTGCTGCTACTCTCTGAAAGCCAGCTGAGCAACAGAGACTGCTGCAGGTG 131
 QY 121 GAGAACTGCACCCAGCTGCGGGAGCAGTGTGAGACCGCGGCATCCCGCAGTTGGCCCTC 180
 Db 132 GAGAACTGCACCCAGCTGCGGGAGCAGTGTGAGACCGCGGCATCCCGCAGTTGGCCCTC 191
 QY 181 CTGACCGTCATCAGCAAAAGGCTGCAGC 207
 Db 192 CTGACCGTCATCAGCAAAAGGCTGCAGC 218

RESULT 11
 ID ABQ83853 standard; cdna; 990 BP.
 XX ABQ83853;
 XX 03-FEB-2003 (first entry)
 XX Human PSCA encoding cdna SEQ ID NO:87.
 XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
 XX T cell; gene; ss.
 XX Homo sapiens.
 XX WO200281646-A2.
 XX 17-OCT-2002.
 XX 04-APR-2002; 2002WO-US011101.
 XX 06-APR-2001; 2001US-0282211P.
 XX 07-NOV-2001; 2001US-0337017P.
 XX 07-MAR-2002; 2002US-0363210P.
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX Sinard JJJ, Diamond DC, Liu L, Xie Z;
 XX WPI; 2003-067518/06.
 XX P-PSDB; ABP74203.
 XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
 XX encoding the peptides, that are useful epitopes of target-associated
 XX antigens.

Claim 1; Page 164-165; 352pp; English.
 The present invention describes an isolated epitope (I) and an epitope
 cluster. Also described is a vaccine or immunotherapeutic composition
 (VC) comprising (I). (I) has cytostatic activity. VC is useful for
 treating an animal, by administering to an animal the vaccine or
 immunotherapeutic composition. VC is also useful for evaluating
 immunogenicity of a vaccine or immunotherapeutic composition, by
 administering VC to an HLA-transgenic animal and evaluating
 immunogenicity based on a characteristic of the animal, or by in vitro
 primary stimulation of a T cell and evaluating immunogenicity. (I) is
 useful for determining specific T cell frequency, by contacting T cells
 with a MHC-peptide complex, and further comprises ELISPOT analysis,
 limiting dilution analysis, flow cytometry, in situ hybridisation and/or
 polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
 ABP74173 represent sequences used in the exemplification of the present
 invention

Sequence 990 BP; 193 A; 299 C; 285 G; 202 T; 0 U; 11 Other;
 Query Match 100.0%; Score 207; DB 7; Length 990;

Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACCATGAAGCTGTGCTGCTTGGCCCTGTGATGCGAGCTTGGCCCTGCAGCCAGCG 60
 Db 12 GTGACCATGAAGCTGTGCTGCTTGGCCCTGTGATGCGAGCTTGGCCCTGCAGCCAGCG 71
 QY 61 ACTGCCCTGCTGCTACTCTCTGAAAGCCAGCTGAGCAACAGAGACTGCTGCAGGTG 120
 Db 72 ACTGCCCTGCTGCTACTCTCTGAAAGCCAGCTGAGCAACAGAGACTGCTGCAGGTG 131
 QY 121 GAGAACTGCACCCAGCTGCGGGAGCAGTGTGAGACCGCGGCATCCCGCAGTTGGCCCTC 180
 Db 132 GAGAACTGCACCCAGCTGCGGGAGCAGTGTGAGACCGCGGCATCCCGCAGTTGGCCCTC 191
 QY 181 CTGACCGTCATCAGCAAAAGGCTGCAGC 207
 Db 192 CTGACCGTCATCAGCAAAAGGCTGCAGC 218

RESULT 12
 ID ADC09589 standard; DNA; 990 BP.
 XX ADC09589;
 XX 18-DEC-2003 (first entry)
 XX PSCA cdna #SEQ ID 87.
 XX Epitope; immunological; vaccine;
 XX major histocompatibility complex class I; MHC class I; cancer;
 XX immunisation; gs.
 XX Unidentified.
 XX WO2003008537-A2.
 XX 30-JAN-2003.
 XX 29-MAR-2002; 2002WO-US010189.
 XX 06-APR-2001; 2001US-0282211P.
 XX 07-NOV-2001; 2001US-0337017P.
 XX 07-MAR-2002; 2002US-0363210P.
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX Sinard JJJ, Diamond DC, Liu L, Xie Z;
 XX WPI; 2003-248010/24.

Epitope having high affinity for major histocompatibility complex class I
 useful for treating an animal, evaluating immunogenicity of a vaccine or
 therapeutic composition and for diagnosing a disease.

Claim 1; SEQ ID NO 87; 239pp; English.

The invention relates to an isolated epitope polypeptide that has high
 affinity for major histocompatibility complex (MHC) class I, and an
 epitope cluster comprising the polypeptide. Also disclosed is a vaccine
 or immunotherapeutic composition containing an epitope of the invention.
 Compositions of the invention may be used in the treatment of cancer. The
 method can be combined with a radiation therapy, chemotherapy,
 biochemotherapy or surgery. The composition is also useful for evaluating
 immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
 peptide complexes of the invention are useful for determining specific T
 cell frequency. This method is useful for evaluating immunological
 response, by performing the method prior to and subsequent to an
 immunisation step. Compositions of the invention are useful for
 diagnosing a disease. The current sequence represents an epitope of the
 invention with high affinity for MHC class I.


```
PR 20-JUL-1999; 99US-00359326.
PR 03-MAY-2000; 2000US-00564329.
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (UROC-) UROGENESYS.
XX PI Reiter R, Witte O, Saffran DC, Jakobovits A;
XX DR WPI; 2001-159478/16.
XX DR P-PSDB; AAB35285.
XX PT Antibodies binding to prostate stem cell antigen inhibit the growth of
XX PT cancer cells and are used to detect and treat prostate, pancreatic or
XX PT bladder cancers.
XX PS Example 1; Fig 1A; 229pp; English.
XX CC The present invention describes a method of treating cancer associated
XX CC with prostate stem cell antigen (PSCA) by administering an antibody which
XX CC selectively binds to PSCA and inhibits the growth of the cancer cells.
XX CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
XX CC the human and murine PSCA protein and coding sequences, which can be used
XX CC not only in the treatment of, but also in detection and prognosis of
XX CC prostate cancer
XX CC
XX CC Sequence 998 BP; 201 A; 299°C; 285 G; 202 T; 0 U; 11 Other;
XX CC
XX CC Query Match 100.0%; Score 207; DB 5; Length 998;
XX CC Best Local Similarity 100.0%; Pred. No. 1.9e-40;
XX CC Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC 1 GTGACCATGAAGGCTGTGCTGCTTGGCCCTTTGATGCGAGGCTGGCCCTGCAGCCAGGC 60
XX CC 12 GTGACCATGAAGGCTGTGCTGCTTGGCCCTTTGATGCGAGGCTGGCCCTGCAGCCAGGC 71
XX CC
XX CC 61 ACTGCCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAAGGAGTGCCTGCAGGTG 120
XX CC 72 ACTGCCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAAGGAGTGCCTGCAGGTG 131
XX CC
XX CC 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGAGCAGCGCGCATCCGCGCAGTTGCGCTC 180
XX CC 132 GAGAACTGCACCCAGCTGGGGAGCAGTGTGAGCAGCGCGCATCCGCGCAGTTGCGCTC 191
XX CC
XX CC 181 CTGACCGTCTATCAGCAAGGCTGCAGC 207
XX CC 192 CTGACCGTCTATCAGCAAGGCTGCAGC 218
XX CC
XX CC RESULT 15
XX CC AAV80397
XX CC ID AAV80397 standard; DNA; 1023 BP.
XX CC AC AAV80397;
XX CC DT 23-FEB-1999 (first entry)
XX CC
XX CC Consensus nucleotide sequence of Utl16 gene.
XX CC
XX CC Utl16; urinary tract; epitope; antigen; detection; diagnosing;
XX CC monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
XX CC metastasis; ss.
XX CC
XX CC Homo sapiens.
XX CC
XX CC Key Location/Qualifiers
XX CC 58..429
XX CC /*tag=
XX CC /product= "Utl16 polypeptide"
XX CC
XX CC WO9851824-A1.
XX CC PD 19-NOV-1998.
XX CC
```

```
PF 15-MAY-1998; 98WO-US009972.
XX PR 15-MAY-1997; 97US-00856652.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
XX PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
XX PI Stroupe SD;
XX DR WPI; 1999-045237/04.
XX DR P-PSDB; AAW86024.
XX PT New method for detecting diseases of the urinary tract - comprises use of
XX PT a Utl16 polynucleotide, protein or antibodies, used for preventing and
XX PT treating urinary tract infections and cancer.
XX PS Claim 1; Fig 1A-C; 113pp; English.
XX CC This represents the consensus nucleotide sequence of the Utl16 gene. The
XX CC invention relates to a method of detecting the presence of a target Utl16
XX CC polynucleotide in a test sample using Utl16-specific sequences (AAV80386
XX CC to AAV80397). Host cells transfected with an expression vector containing
XX CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
XX CC This polypeptide has at least one Utl16 epitope which can be used in a
XX CC method for detecting Utl16 antigen in a test sample. The polynucleotides
XX CC and polypeptides are useful for detecting, diagnosing, monitoring,
XX CC staging, prognosticating, in vivo imaging, preventing, treating or
XX CC determining the predisposition of a subject to diseases and conditions of
XX CC the urinary tract, such as urinary tract cancer. Antibodies specifically
XX CC binding to an epitope of Utl16 antigen, and agonists are useful for
XX CC treating urinary tract diseases, tumours and metastases
XX CC
XX CC Sequence 1023 BP; 194 A; 350 C; 288 G; 191 T; 0 U; 0 Other;
XX CC
XX CC Query Match 100.0%; Score 207; DB 2; Length 1023;
XX CC Best Local Similarity 100.0%; Pred. No. 1.9e-40;
XX CC Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC 1 GTGACCATGAAGGCTGTGCTGCTTGGCCCTTTGATGCGAGGCTGGCCCTGCAGCCAGGC 60
XX CC 52 GTGACCATGAAGGCTGTGCTGCTTGGCCCTTTGATGCGAGGCTGGCCCTGCAGCCAGGC 111
XX CC
XX CC 61 ACTGCCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAAGGAGTGCCTGCAGGTG 120
XX CC 112 ACTGCCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAAGGAGTGCCTGCAGGTG 171
XX CC
XX CC 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGAGCAGCGCGCATCCGCGCAGTTGCGCTC 180
XX CC 172 GAGAACTGCACCCAGCTGGGGAGCAGTGTGAGCAGCGCGCATCCGCGCAGTTGCGCTC 231
XX CC
XX CC 181 CTGACCGTCTATCAGCAAGGCTGCAGC 207
XX CC 232 CTGACCGTCTATCAGCAAGGCTGCAGC 258
XX CC
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Search completed: September 18, 2004, 07:06:57
Job time : 136.318 secs

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Result No.	Query			ID	Description
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2	207	100.0	494	2	Sequence 23, Appl
3	207	100.0	998	3	Sequence 4, Appl
4	207	100.0	998	3	Sequence 1, Appl
5	207	100.0	998	3	Sequence 1, Appl
6	207	100.0	998	3	Sequence 1, Appl
7	207	100.0	998	4	Sequence 1, Appl
8	195.8	94.6	232	2	Sequence 1, Appl
9	190	91.8	960	2	Sequence 25, Appl
10	190	91.8	960	4	Sequence 17, Appl
11	190	91.8	960	4	Sequence 17, Appl
12	159	76.8	286	2	Sequence 17, Appl
13	103.4	50.0	441	3	Sequence 21, Appl
14	103.4	50.0	441	3	Sequence 3, Appl
15	103.4	50.0	441	3	Sequence 3, Appl
16	103.4	50.0	441	3	Sequence 3, Appl
17	103.4	50.0	441	4	Sequence 3, Appl
18	52.4	25.3	280	2	Sequence 17, Appl
19	52.2	25.2	262	2	Sequence 10, Appl
20	52.2	25.2	289	2	Sequence 11, Appl
21	52.2	25.2	537	2	Sequence 3, Appl
22	52.2	25.2	1066	1	Sequence 3, Appl
23	52.2	25.2	1095	2	Sequence 1, Appl
24	52.2	25.2	1163	3	Sequence 1, Appl
25	51.2	24.7	266	2	Sequence 16, Appl
26	51.2	24.7	335	2	Sequence 12, Appl
27	46.8	22.6	996	2	Sequence 8, Appl

QY 61 ACTGCCCTGCTGTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTCAGGTG 120
Db 61 ACTGCCCTGCTGTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTCAGGTG 120
QY 121 GAGAACTGACCCAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCAGTTGGCCTC 180
Db 121 GAGAACTGACCCAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCAGTTGGCCTC 180
QY 181 CTGACCGTATCATGACCAAGCTGCAGC 207
Db 181 CTGACCGTATCATGACCAAGCTGCAGC 207

RESULT 2
US-08-675-508-4
; Sequence 4, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,508
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Ballings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0355
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SCMH-2
; CLONE:
; US-08-675-508-4

Query Match 100.0%; Score 207; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTCAGCCAGGC 60
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QY 61 ACTGCCCTGCTGTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTCAGGTG 120
Db 61 ACTGCCCTGCTGTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTCAGGTG 120
QY 121 GAGAACTGACCCAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCAGTTGGCCTC 180
Db 121 GAGAACTGACCCAGTGGGGAGCAGTCTGGACCGCGCATCCGCGCAGTTGGCCTC 180
QY 181 CTGACCGTATCATGACCAAGCTGCAGC 207

Db 181 CTGACCGTATCATGACCAAGGCTGCAGC 207

RESULT 3
US-09-203-939-1
; Sequence 1, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (604)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (615)
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; US-09-203-939-1

Query Match 100.0%; Score 207; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTCAGCCAGGC 60
Db 12 GTGACCATGAAGGCTGTGCTGCTTCCCTGTGTGATGGCAGGCTTGGCCCTCAGCCAGGC 71
QY 61 ACTGCCCTGCTGTGCTACTCTGCAAGCCAGGTGAGCAACGAGGACTGCTTCAGGTG 120

Db 72 ACTGCCCTGCTGCTACTCTCTGCAAGCCAGGTGAGCAAGAGGAGTGCCTGCAGGTG 131
QY 121 GAGAACTGACACCGAGTGGGAGGAGTCTGGACCGGCGCATCCGGCAGTTGGGCTC 180
Db 132 GAGAACTGACACCGAGTGGGAGGAGTCTGGACCGGCGCATCCGGCAGTTGGGCTC 191
QY 181 CTGACCGTCAATCAGCAAAAGGCTGCAGC 207
Db 192 CTGACCGTCAATCAGCAAAAGGCTGCAGC 218

RESULT 4

US-09-251-835-1
; Sequence 1, Application US/09251835A
; Patent No. 6261789
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US12
; CURRENT APPLICATION NUMBER: US/09/251,835A
; CURRENT FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)

US-09-251-835-1

Query Match 100.0%; Score 207; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACCATGAGGCTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
Db 12 GTGACCATGAGGCTGCTGCTTGCCTTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTGCTGCTACTCTCTGCAAAAGGCTGCAGC 207
Db 72 ACTGCCCTGCTGCTACTCTCTGCAAAAGGCTGCAGC 218
QY 121 GAGAACTGACACCGAGTGGGAGGAGTCTGGACCGGCGCATCCGGCAGTTGGGCTC 180
Db 132 GAGAACTGACACCGAGTGGGAGGAGTCTGGACCGGCGCATCCGGCAGTTGGGCTC 191
QY 181 CTGACCGTCAATCAGCAAAAGGCTGCAGC 207
Db 192 CTGACCGTCAATCAGCAAAAGGCTGCAGC 218

RESULT 5

US-09-318-503-1
; Sequence 1, Application US/09318503A
; Patent No. 6261791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318,503A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 60/074,675
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:

NAME/KEY: misc_feature
 LOCATION: (615)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (636)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (640)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (646)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (697)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (926)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 US-09-318-503-1

Query Match 100.0%; Score 207; DB 3; Length 998;
 Best Local Similarity 100.0%; Pred. No. 2.1e-44;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
 Db 12 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
 QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGAGGATGCTGCAGGTG 120
 Db 72 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGAGGATGCTGCAGGTG 131
 QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGTCAGCCGGCGCATCCGGCGAGTTGGCCCTC 180
 Db 132 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGTCAGCCGGCGCATCCGGCGAGTTGGCCCTC 191
 QY 181 CTGACCGTCATCAGCAAAAGGCTGCAGC 207
 Db 192 CTGACCGTCATCAGCAAAAGGCTGCAGC 218

RESULT 6
 US-09-038-261A-1
 ; Sequence 1, Application US/09038261A
 ; Patent No. 6267960
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
 ; FILE REFERENCE: 30435.54USU1
 ; CURRENT APPLICATION NUMBER: US/09/038,261A
 ; CURRENT FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 998
 ; TYPE: DNA
 ; ORGANISM: HUMAN PSCA (hPSCA)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (543)
 ; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature
 LOCATION: (580)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (584)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (604)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (608)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (615)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (636)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (640)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (646)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 NAME/KEY: misc_feature
 LOCATION: (926)
 OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
 US-09-038-261A-1

Query Match 100.0%; Score 207; DB 3; Length 998;
 Best Local Similarity 100.0%; Pred. No. 2.1e-44;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
 Db 12 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71
 QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGAGGATGCTGCAGGTG 120
 Db 72 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGAGGATGCTGCAGGTG 131
 QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGTCAGCCGGCGCATCCGGCGAGTTGGCCCTC 180
 Db 132 GAGAACTGCACCCAGCTGGGGGAGCAGTCTGTCAGCCGGCGCATCCGGCGAGTTGGCCCTC 191
 QY 181 CTGACCGTCATCAGCAAAAGGCTGCAGC 207
 Db 192 CTGACCGTCATCAGCAAAAGGCTGCAGC 218

RESULT 7
 US-09-564-329A-1
 ; Sequence 1, Application US/09564329A
 ; Patent No. 6541212
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/09/564,329A
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13

APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 17
LENGTH: 960
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-794A-17

Query Match 91.8%; Score 190; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 4.8e-40;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTA 77
Db 1 GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTA 60
QY 78 CTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTTGCAGTGGAGAACTGCACCCAGCT 137
Db 61 CTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCTTGCAGTGGAGAACTGCACCCAGCT 120
QY 138 GGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGGCTCTGACCGTCAACAGCAA 197
Db 121 GGGGAGCAGTGTGGACCGCGGCATCCGCGCAGTTGGCTCTGACCGTCAACAGCAA 180
QY 198 AGGCTGCAGC 207
Db 181 AGGCTGCAGC 190
RESULT 10
US-09-905-125A-17
Sequence 17, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-17

Query Match
Best Local Similarity 91.8%; Score 190; DB 4; Length 960;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCTGCTTGCCTGTTGATGCGCAGGCTTGGCCCTGCGAGGCACTGCGCCCTGCTGTGCTA 77
Db 1 GCTGCTTGCCTGTTGATGCGCAGGCTTGGCCCTGCGAGGCACTGCGCCCTGCTGTGCTA 60

QY 78 CTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGTGGGAGTGGAGCACTGCACTT 137
Db 61 CTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGTGGGAGTGGAGCACTGCACTT 120

QY 138 GGGGAGCAGTGTGACCGCGGCATCCGCGAGTGGCCCTGCGAGTGGAGCACTGCACTT 197
Db 121 GGGGAGCAGTGTGACCGCGGCATCCGCGAGTGGCCCTGCGAGTGGAGCACTGCACTT 180

QY 198 AGGCTGCAGC 207
Db 181 AGGCTGCAGC 190

RESULT 11
US-09-902-775A-17
; Sequence 17, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902, 775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-17

Query Match
Best Local Similarity 91.8%; Score 190; DB 4; Length 960;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCTGCTTGCCTGTTGATGCGCAGGCTTGGCCCTGCGAGGCACTGCGCCCTGCTGTGCTA 77
Db 1 GCTGCTTGCCTGTTGATGCGCAGGCTTGGCCCTGCGAGGCACTGCGCCCTGCTGTGCTA 60

QY 78 CTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGTGGGAGTGGAGCACTGCACTT 137
Db 61 CTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCGAGTGGGAGTGGAGCACTGCACTT 120

QY 138 GGGGAGCAGTGTGACCGCGGCATCCGCGAGTGGCCCTGCGAGTGGAGCACTGCACTT 197
Db 121 GGGGAGCAGTGTGACCGCGGCATCCGCGAGTGGCCCTGCGAGTGGAGCACTGCACTT 180

QY 198 AGGCTGCAGC 207
Db 181 AGGCTGCAGC 190

RESULT 12
US-08-675-508-21
; Sequence 21, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS

Db 181 GTTATCAGTAGGGCTGCAGC 201

RESULT 15
US-09-318-503-3
; Sequence 3, Application US/09318503A
; Patent No. 6281791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435-54US13
; CURRENT APPLICATION NUMBER: US/09/318,503A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 60/074,675
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)
US-09-318-503-3

Query Match 50.0%; Score 103.4; DB 3; Length 441;
Best Local Similarity 69.7%; Pred. No. 6.2e-18;
Matches 140; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY	7	ATGAAGCTGTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCC	66
Db	1	ATGAAGACAGTTTTTTTATCTCTGCGCCACCTATTAGCCCTGCATCCAGGTGCTGCT	60
QY	67	CTGCTGTGCTACTCCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTGGAGAAC	126
Db	61	CTGCAGTGTCTATTTCATGCACAGCACAGATGACACACAGAGACTGTCTGAATGTACAGAAC	120
QY	127	TGCACCCAGCTGGGGGAGCAGTCTGGACCGCGCGCATCCGGCAGTTGGCCTCCTGACC	186
Db	121	TGCAGCCTGGACACAGACAGTTCCTTTTACATCCGGCATCCGGCCATTGGACTCTGTGACA	180
QY	187	GTATCAGCAAGGCTGCAGC	207
Db	181	GTTATCAGTAAGGGCTGCAGC	201

Search completed: September 18, 2004, 19:23:19
Job time : 25.1818 secs

Blank sheet

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: September 18, 2004, 06:17:58 : Search time 155,136 Seconds
(without alignments)
6734.858 Million cell updates/sec

Title: US-09-079-874-4
Perfect score: 207
Sequence: 1 GTGACCATGAGGCTGTGCT.....TCATCAGCAAGGCTGCAGC 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues
Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				Published Applications NA:*	
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3:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:			3:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
4:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:			4:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
5:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:			5:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
6:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:			6:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
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12:	/cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:			12:	/cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:
13:	/cgn2_6/ptodata/2/pubpna/US09F_PUBCOMB.seq:			13:	/cgn2_6/ptodata/2/pubpna/US09F_PUBCOMB.seq:
14:	/cgn2_6/ptodata/2/pubpna/US09G_PUBCOMB.seq:			14:	/cgn2_6/ptodata/2/pubpna/US09G_PUBCOMB.seq:
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18:	/cgn2_6/ptodata/2/pubpna/US09K_PUBCOMB.seq:			18:	/cgn2_6/ptodata/2/pubpna/US09K_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	207	100.0	279	11	Sequence 4, Appli
3	207	100.0	288	11	Sequence 3, Appli
4	207	100.0	293	11	Sequence 23, Appl
5	207	100.0	494	9	US-09-080-140-2
6	207	100.0	990	13	US-09-934-586A-4
7	207	100.0	990	16	Sequence 386, App
8	207	100.0	990	17	US-10-240-425-386
9	207	100.0	990	17	Sequence 87, Appl
10	207	100.0	998	9	US-10-117-937-87
11	207	100.0	998	9	Sequence 168, App
12	207	100.0	998	9	Sequence 1, Appli
13	207	100.0	998	9	Sequence 1, Appli
14	207	100.0	998	9	Sequence 1, Appli
15	207	100.0	998	9	Sequence 1, Appli
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41	207	100.0	998	9	Sequence 1, Appli
42	207	100.0	998	9	Sequence 1, Appli
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15	207	100.0	998	15	US-10-225-784-1
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18	207	100.0	998	16	US-10-374-381-1
19	207	100.0	998	16	US-10-446-542-1
20	207	100.0	1023	11	US-09-080-140-11
21	207	100.0	1023	11	US-09-080-140-12
22	207	100.0	1028	15	US-10-252-157-273
23	198	95.7	290	11	US-09-080-140-1
24	195.8	94.6	222	9	US-09-934-586A-25
25	190	91.8	960	9	US-09-909-320-17
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27	190	91.8	960	9	US-09-905-291A-17
28	190	91.8	960	9	US-09-902-853-17
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31	190	91.8	960	10	US-09-904-011-17
32	190	91.8	960	10	US-09-906-742-17
33	190	91.8	960	10	US-09-906-838-17
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35	190	91.8	960	10	US-09-907-942-17
36	190	91.8	960	10	US-09-904-859-17
37	190	91.8	960	10	US-09-909-204-17
38	190	91.8	960	10	US-09-904-820-17
39	190	91.8	960	10	US-09-904-788-17
40	190	91.8	960	10	US-09-906-646-17
41	190	91.8	960	10	US-09-906-700-17
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43	190	91.8	960	10	US-09-902-903-17
44	190	91.8	960	10	US-09-903-749A-17
45	190	91.8	960	10	US-09-904-119-17

ALIGNMENTS

RESULT 1
US-09-080-140-4
; Sequence 4, Application US/09080140
; Publication No. US20040018553A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,140
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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/
/ APPLICATION NUMBER: 08/856,653
/ FILING DATE: 15-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Becker, Cheryl L.
/ REGISTRATION NUMBER: 35,441
/ REFERENCE/DOCKET NUMBER: 6105.US.PI
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 847/935-1729
/ TELEFAX: 847/938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 207 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-080-140-4

Query Match 100.0%; Score 207; DB 11; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.1e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
Db 1 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGGACTGCTGCAGGTG 120
Db 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGGACTGCTGCAGGTG 120
QY 121 GAGAATGCACCCAGCTGGGGGAGCAGTCTGCACCGCGCGCATCCGGCGAGTTGGCCCTC 180
Db 121 GAGAATGCACCCAGCTGGGGGAGCAGTCTGCACCGCGCGCATCCGGCGAGTTGGCCCTC 180
QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
Db 181 CTGACCGTCATCAGCAAGGCTGCAGC 207

RESULT 2
US-09-080-140-3
/ Sequence 3, Application US/09080140
/ Publication No. US20040018553A1
/ GENERAL INFORMATION:
/ APPLICANT: BILLING-MEDEL, PATRICIA
/ APPLICANT: COHEN MAURICE
/ APPLICANT: COLPITTS, TRACEY L.
/ APPLICANT: FRIEDMAN, PAULA N.
/ APPLICANT: GORDON, JULIAN
/ APPLICANT: GRANADOS, EDWARD N.
/ APPLICANT: HODGES, STEVEN C.
/ APPLICANT: KLASS, MICHAEL R.
/ APPLICANT: KRTOCHVIL, JON D.
/ APPLICANT: ROBERTS-RAPP, LISA
/ APPLICANT: RUSSELL, JOHN C.
/ APPLICANT: STROUPE, STEPHEN D.
/ TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
/ FOR DETECTING DISEASES OF THE PROSTATE
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Abbott Laboratories
/ STREET: 100 Abbott Park Road
/ CITY: Abbott Park
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09080,140

/
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/856,653
/ FILING DATE: 15-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Becker, Cheryl L.
/ REGISTRATION NUMBER: 35,441
/ REFERENCE/DOCKET NUMBER: 6105.US.PI
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 847/935-1729
/ TELEFAX: 847/938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 279 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-080-140-3

Query Match 100.0%; Score 207; DB 11; Length 279;
Best Local Similarity 100.0%; Pred. No. 7.2e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
Db 3 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 62
QY 61 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGGACTGCTGCAGGTG 120
Db 63 ACTGCCCTCTGTGCTACTCTCTGCAAGCCAGGTGAGCAAGGACTGCTGCAGGTG 122
QY 121 GAGAATGCACCCAGCTGGGGGAGCAGTCTGCACCGCGCGCATCCGGCGAGTTGGCCCTC 180
Db 123 GAGAATGCACCCAGCTGGGGGAGCAGTCTGCACCGCGCGCATCCGGCGAGTTGGCCCTC 182
QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
Db 183 CTGACCGTCATCAGCAAGGCTGCAGC 209

RESULT 3
US-09-934-586A-23
/ Sequence 23, Application US/09934586A
/ Patent No. US20020058241A1
/ GENERAL INFORMATION:
/ APPLICANT: Au-Young, Janice
/ TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: U.S.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/934,586A
/ FILING DATE: 23-Aug-2001
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/225,080
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0066 US
/ TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT02
; CLONE: 1312529
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-934-586A-23

Query Match 100.0%; Score 207; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.2e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 1 GTGACCATGAAGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
QY 61 ACTGCCCTGCTGCTGCTGCTTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 120
DB 61 ACTGCCCTGCTGCTGCTGCTTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 120
QY 121 GAGAACTGACCCAGCTGGGGAGAGCTGCTGAGCGGGCGCATCGGCGCAGTTGGCCTC 180
DB 121 GAGAACTGACCCAGCTGGGGAGAGCTGCTGAGCGGGCGCATCGGCGCAGTTGGCCTC 180
QY 181 CTGACCGTCTCATCAGCAAGGCTGCAGC 207
DB 181 CTGACCGTCTCATCAGCAAGGCTGCAGC 207

RESULT 4
US-09-080-140-2
; Sequence 2, Application US/09080140
; Publication No. US20040018553A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,140
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT02
; CLONE: 1312529
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-934-586A-23

Query Match 100.0%; Score 207; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.2e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 1 GTGACCATGAAGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
QY 61 ACTGCCCTGCTGCTGCTGCTTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 120
DB 61 ACTGCCCTGCTGCTGCTGCTTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 120
QY 121 GAGAACTGACCCAGCTGGGGAGAGCTGCTGAGCGGGCGCATCGGCGCAGTTGGCCTC 180
DB 121 GAGAACTGACCCAGCTGGGGAGAGCTGCTGAGCGGGCGCATCGGCGCAGTTGGCCTC 180
QY 181 CTGACCGTCTCATCAGCAAGGCTGCAGC 207
DB 181 CTGACCGTCTCATCAGCAAGGCTGCAGC 207

RESULT 5
US-09-934-586A-4
; Sequence 4, Application US/09934586A
; Patent No. US20020058241A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/934,586A
; FILING DATE: 23-Aug-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/225,080
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; APPLICATION NUMBER: 08/856,653
; FILING DATE: 15-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6105.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-080-140-2

Query Match 100.0%; Score 207; DB 11; Length 293;
Best Local Similarity 100.0%; Pred. No. 7.2e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCCAGGC 60
DB 27 GTGACCATGAAGCTGTGCTGCTTCCCTGCTGATGGCAGGCTTGGCCCTGCAGCCAGGC 86
QY 61 ACTGCCCTGCTGCTGCTTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 120
DB 87 ACTGCCCTGCTGCTGCTTCTCTGCAAGCCAGGTCAGCAACGAGGACTGCTGCAGGTG 146
QY 121 GAGAACTGACCCAGCTGGGGAGAGCTGCTGAGCGGGCGCATCGGCGCAGTTGGCCTC 180
DB 147 GAGAACTGACCCAGCTGGGGAGAGCTGCTGAGCGGGCGCATCGGCGCAGTTGGCCTC 206
QY 181 CTGACCGTCTCATCAGCAAGGCTGCAGC 207
DB 207 CTGACCGTCTCATCAGCAAGGCTGCAGC 233
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Db 192 CTGACCGTCATCAGCAAGGCTGCAGC 218

RESULT 10

US-09-855-153-1

Sequence 1, Application US/09855153

Patent No. US20020102666A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT APPLICATION NUMBER: US/09/855,153

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: 09/564,329

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 08/814,279

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: 60/074,675

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: 60/120,536

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 60/124,658

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/038,261

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 09/203,939

PRIOR FILING DATE: 1998-12-02

PRIOR APPLICATION NUMBER: 09/251,835

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 09/308,503

PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 998

TYPE: DNA

ORGANISM: HUMAN PSCA (hPSCA)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (543)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (580)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (584)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (604)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (608)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (615)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (636)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (640)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (646)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (697)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (926)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

US-09-855-153-1

Query Match 100.0%; Score 207; DB 9; Length 998;

Best Local Similarity 100.0%; Pred No. 7.5e-52; Mismatches 0; Indels 0; Gaps 0;

Matches 207; Conservative 0;

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Db 12 GTGACCATGAAGGCTGTGCTTGGCCCTTGTATGCGAGGCTTGCCCTGCAGCCAGGC 71

Qy 61 ACTGCCCTGTGTCTACTCTCTCAAGCCAGGTGAGCAACGAGCACTGCCTGCAGGTG 120

Db 72 ACTGCCCTGTGTCTACTCTCTCAAGCCAGGTGAGCAACGAGCACTGCCTGCAGGTG 131

Qy 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCATCCGCGAGTTGCCCTC 180

Db 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTCTGACCGCGCATCCGCGAGTTGCCCTC 191

Qy 181 CTGACCGTCATCAGCAAGGCTGCAGC 207

Db 192 CTGACCGTCATCAGCAAGGCTGCAGC 218

RESULT 11

US-09-854-811-1

Sequence 1, Application US/09854811

Patent No. US20020119157A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT APPLICATION NUMBER: US/09/854,811

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: 09/564,329

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR FILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 998

TYPE: DNA

ORGANISM: HUMAN PSCA (hPSCA)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (543)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (580)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (584)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (604)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (608)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (615)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)

NAME/KEY: misc_feature

LOCATION: (636)

OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)


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; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-854-811-1

Query Match      100.0%; Score 207; DB 9; Length 998;
Best Local Similarity 100.0%; Pred. No. 7.5e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCAGGC 60
Db 12 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCAGGC 71

QY 61 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120
Db 72 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 131

QY 121 GAGAACTGCACCACTGGGGAGCAGTGTGACCGCGGCATCCGCGCAGTTGGCCTC 180
Db 132 GAGAACTGCACCACTGGGGAGCAGTGTGACCGCGGCATCCGCGCAGTTGGCCTC 191

QY 181 CTGACCGTCAATCAGCAAGGCTGCAGC 207
Db 192 CTGACCGTCAATCAGCAAGGCTGCAGC 218
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RESULT 12
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; Sequence 1, Application US/09934773
; Patent No. US20020136689A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/934,773
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
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; NAME/KEY: misc feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-934-773-1

Query Match      100.0%; Score 207; DB 9; Length 998;
Best Local Similarity 100.0%; Pred. No. 7.5e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCAGGC 60
Db 12 GTGACCATGAAGGCTGTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCAGGC 71

QY 61 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120
Db 72 ACTGCCCTGTGCTTACTCTCTGCAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 131

QY 121 GAGAACTGCACCACTGGGGAGCAGTGTGACCGCGGCATCCGCGCAGTTGGCCTC 180
Db 132 GAGAACTGCACCACTGGGGAGCAGTGTGACCGCGGCATCCGCGCAGTTGGCCTC 191

QY 181 CTGACCGTCAATCAGCAAGGCTGCAGC 207
Db 192 CTGACCGTCAATCAGCAAGGCTGCAGC 218
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RESULT 13
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; Sequence 1, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
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	PRIOR FILING DATE:	2000-05-03	
	PRIOR APPLICATION NUMBER:	09/359,326	
	PRIOR FILING DATE:	1999-07-20	
	PRIOR APPLICATION NUMBER:	08/814,279	
	PRIOR FILING DATE:	1997-03-10	
	PRIOR APPLICATION NUMBER:	60/071,141	
	PRIOR FILING DATE:	1998-01-12	
	PRIOR APPLICATION NUMBER:	60/074,675	
	PRIOR FILING DATE:	1998-02-13	
	PRIOR APPLICATION NUMBER:	60/113,230	
	PRIOR FILING DATE:	1998-12-21	
	PRIOR APPLICATION NUMBER:	60/120,536	
	PRIOR FILING DATE:	1999-02-17	
	PRIOR APPLICATION NUMBER:	60/124,658	
	PRIOR FILING DATE:	1999-03-16	
	PRIOR APPLICATION NUMBER:	09/038,261	
	PRIOR FILING DATE:	1998-03-10	
	PRIOR APPLICATION NUMBER:	09/203,939	
	PRIOR FILING DATE:	1998-12-02	
	PRIOR APPLICATION NUMBER:	09/251,835	
	PRIOR FILING DATE:	1999-02-17	
	PRIOR APPLICATION NUMBER:	09/308,503	
	PRIOR FILING DATE:	1999-05-25	
	NUMBER OF SEQ ID NOS:	27	
	SOFTWARE:	Patentin Ver. 2.0	
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	LENGTH:	998	
	TYPE:	DNA	
	ORGANISM:	HUMAN PSCA (hPSCA)	
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	LOCATION:	{543}	
	OTHER INFORMATION:	any nucleotide (i.e., a, c, g or t)	
	NAME/KEY:	misc feature	
	LOCATION:	{580}	
	OTHER INFORMATION:	any nucleotide (i.e., a, c, g or t)	
	NAME/KEY:	misc feature	
	LOCATION:	{584}	
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	LOCATION:	{604}	
	OTHER INFORMATION:	any nucleotide (i.e., a, c, g or t)	
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	US-09-963-620-1		
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	Matches 207; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	GTGACCATGAAGCTGTGCTTGGCCCTTTGATGGCAGGCTTGCCCTCGACCGCAGGC	60
Db	12	GTGACCATGAAGCTGTGCTTGGCCCTTTGATGGCAGGCTTGCCCTCGACCGCAGGC	71

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; LOCATION: {615}
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc_feature
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; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-855-632-1

Query Match      100.0%; Score 207; DB 10; Length 998;
Best Local Similarity 100.0%; Pred. No. 7,5e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 12 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71

QY 61 ACTGCCCTGTGCTGCTACTCTCTGCAAGCCAGGCTGAGCAACGAGGACTGCTTGCAGGTG 120
DB 72 ACTGCCCTGTGCTGCTACTCTCTGCAAGCCAGGCTGAGCAACGAGGACTGCTTGCAGGTG 131

QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGTGACCCGCGGATCCGCGAGTTGGCCCTC 180
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; Publication No. US20030113820A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,784
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; TYPE: DNA
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; NAME/KEY: misc_feature
; LOCATION: {543}
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc_feature
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US-10-225-784-1
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Query Match      100.0%; Score 207; DB 15; Length 998;
Best Local Similarity 100.0%; Pred. No. 7,5e-52;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 12 GTGACCATGAAGGCTGTGCTGCTTGGCCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGC 71

QY 61 ACTGCCCTGTGCTGCTACTCTCTGCAAGCCAGGCTGAGCAACGAGGACTGCTTGCAGGTG 120
DB 72 ACTGCCCTGTGCTGCTACTCTCTGCAAGCCAGGCTGAGCAACGAGGACTGCTTGCAGGTG 131

QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGTGACCCGCGGATCCGCGAGTTGGCCCTC 180
DB 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGTGACCCGCGGATCCGCGAGTTGGCCCTC 191

QY 181 CTGACCGTCTATCAGCAAAAGGCTGCAGC 207
DB 192 CTGACCGTCTATCAGCAAAAGGCTGCAGC 218
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Mon Sep 20 09:12:09 2004

us-09-079-874-4.rnpb

Page 10

Search completed: September 18, 2004, 20:20:21
Job time : 158.136 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 05:54:35 ; Search time 946.591 Seconds
(without alignments)
6530.246 Million cell updates/sec

Title: US-09-079-874-4
Perfect score: 207
Sequence: 1 GGCACATGAAGCTGTGCT.....TCATCAGCAAGGCTGCAGC 207

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	207	100.0	827	12	BM018750
9	207	100.0	972	12	BM018834
10	207	100.0	1024	8	BC023582
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ALIGNMENTS

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BM768967
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DEFINITION K-EST0052116 SL4K402 Homo sapiens cdna clone SL4K402-13-D04 5',
424 bp mRNA linear EST 04-MAR-2002
rna sequence.
ACCESSION BM768967
VERSION BM768967.1 GI:19098582
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 424)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 13 row: D column: 04
High quality sequence stop: 424.

CB147558 K-EST0203
BM042219 603616172
EG761095 602717425
BM018750 603646652
BM018834 603646752
BM023582 Homo sapi
BM750435 K-EST0026
BM828076 K-EST0100
CB996183 AGENCOURT
CB997275 AGENCOURT
CB993163 AGENCOURT
BC048808 Homo sapi
BM042052 603615054
EQ678675 AGENCOURT
EQ876328 AGENCOURT
BU179764 AGENCOURT
AY418122 Homo sapi
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BU174241 AGENCOURT
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EG765417 602738887
BU157227 AGENCOURT
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AY418123 Pan trogl
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BI862705 603389882
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FEATURES
source

Location/Qualifiers
1. .424
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="S14K402-13-D04"
/cell_line="K402"
/lab_host="Top10F"
/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 207; DB 12; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.3e-34; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 0;

QY 1 GTGACCATGAAGCTGTGCTTGGCCCTGTTGATGGCAGGCTTGCCCTGCAGCCAGGC 60
DB 52 GTGACCATGAAGCTGTGCTTGGCCCTGTTGATGGCAGGCTTGCCCTGCAGCCAGGC 111
QY 61 ACTGCCCTGTGCTTACTCTCTCAAGCCAGGTGAGCAAGCAGGACTGCTGCAGGTG 120
DB 112 ACTGCCCTGTGCTTACTCTCTCAAGCCAGGTGAGCAAGCAGGACTGCTGCAGGTG 171
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCGCGCGCATCGCGCAGTGTGCGCTC 180
DB 172 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCGCGCGCATCGCGCAGTGTGCGCTC 231
QY 181 CTGACCGTCTATCAGCAAGGCTGCAGC 207
DB 232 CTGACCGTCTATCAGCAAGGCTGCAGC 258

RESULT 2

BQ083505
LOCUS
DEFINITION
BQ083505
VERSION
BQ083505.1 GI:19942340
KEYWORDS
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
REFERENCE
AUTHORS
Oh, K.J., Cheong, J.E., Sohn, H.Y., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, N.S., Hahn, Y., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE
21C Frontier Korean EST Project 2001

JOURNAL
COMMENT
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr

FEATURES
source

Plate: 65 row: D column: 08
High quality sequence stop: 470.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-65-D08"
/cell_line="K402"
/lab_host="Top10F"
/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 207; DB 13; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.4e-34; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 0;

QY 1 GTGACCATGAAGCTGTGCTTGGCCCTTGTATGGCAGGCTTGCCCTGCAGCCAGGC 60
DB 52 GTGACCATGAAGCTGTGCTTGGCCCTTGTATGGCAGGCTTGCCCTGCAGCCAGGC 111
QY 61 ACTGCCCTGTGCTTACTCTCTCAAGCCAGGTGAGCAAGCAGGACTGCTGCAGGTG 120
DB 112 ACTGCCCTGTGCTTACTCTCTCAAGCCAGGTGAGCAAGCAGGACTGCTGCAGGTG 171
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCGCGCGCATCGCGCAGTGTGCGCTC 180
DB 172 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCGCGCGCATCGCGCAGTGTGCGCTC 231
QY 181 CTGACCGTCTATCAGCAAGGCTGCAGC 207
DB 232 CTGACCGTCTATCAGCAAGGCTGCAGC 258

RESULT 3

BM819937
LOCUS
DEFINITION
K-EST0088167 S18N669761 Homo sapiens cDNA clone S18N669761-19-E04
5', mRNA sequence.
BM819937
VERSION
BM819937.1 GI:19176350
KEYWORDS
EST.

ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
REFERENCE
AUTHORS
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE
21C Frontier Korean EST Project 2001

JOURNAL
COMMENT
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470

Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 19 row: E column: 04
 High quality sequence stop: 480.
 Location/Qualifiers
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FEATURES

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 /db_xref="taxon:9606"
 /clone="S18N69761-19-E04"
 /sex="F"
 /lab_host="Top10F"
 /clone_lib="S18N69761"
 /notes="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 207; DB 12; Length 480;
 Best Local Similarity 100.0%; Pred. No. 2.4e-34;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACCATGAAGCTGTGCTGCTTGCCTGTTGATGGCAGGCTTGCCCTGCAGCAGGC 60
 Db 12 GTGACCATGAAGCTGTGCTGCTTGCCTGTTGATGGCAGGCTTGCCCTGCAGCAGGC 71
 QY 61 ACTGCCCTGTGTGCTACTCTCTCAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGGTG 120
 Db 72 ACTGCCCTGTGTGCTACTCTCTCAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGGTG 131
 QY 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCGCGCAGTTGGCCTC 180
 Db 132 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCGCGCAGTTGGCCTC 191
 QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
 Db 192 CTGACCGTCATCAGCAAGGCTGCAGC 218

RESULT 4
 BQ083498
 LOCUS X-EST0146178 S14K402 Homo sapiens cDNA clone S14K402-65-C11 5',
 DEFINITION mRNA sequence.
 ACCESSION BQ083498
 VERSION BQ083498.1 GI:19942325
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 527)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 65 row: C column: 11
 High quality sequence stop: 527.
 Location/Qualifiers
 1. .527

FEATURES

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 /mol_type="mRNA"
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 /clone="S14K402-65-C11"
 /cell_line="K402"
 /lab_host="Top10F"
 /clone_lib="S14K402"
 /notes="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN
 Query Match 100.0%; Score 207; DB 13; Length 527;
 Best Local Similarity 100.0%; Pred. No. 2.5e-34;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACCATGAAGCTGTGCTGCTTGCCTGTTGATGGCAGGCTTGCCCTGCAGCAGGC 60
 Db 52 GTGACCATGAAGCTGTGCTGCTTGCCTGTTGATGGCAGGCTTGCCCTGCAGCAGGC 111
 QY 61 ACTGCCCTGTGTGCTACTCTCTCAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGGTG 120
 Db 112 ACTGCCCTGTGTGCTACTCTCTCAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGGTG 171
 QY 121 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCGCGCAGTTGGCCTC 180
 Db 172 GAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATCGCGCAGTTGGCCTC 231
 QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
 Db 232 CTGACCGTCATCAGCAAGGCTGCAGC 258

RESULT 5
 CB147558
 LOCUS X-EST0203584 L11SNU354s1 Homo sapiens cDNA clone L11SNU354s1-29-C07
 DEFINITION 5', mRNA sequence.
 ACCESSION CB147558
 VERSION CB147558.1 GI:28129015
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 550)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 row: C column: 07
High quality sequence stop: 550.

FEATURES

Source

1. 550
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="L115NU354s1-29-C07"
/sex="M"
/tissue_type="Liver"
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/cell_line="SNU-354"
/lab_host="Top10P"
/clone_lib="L115NU354s1"

/note="Organ: Liver; Vector: pONS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10P with electroporation method."

ORIGIN

Query Match 100.0%; Score 207; DB 14; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 12 GTGACCATGAAGCTGTGCTGTGCTTGCCTTGTGATGGCAGGCTTGCCCTGCAGCCAGGC 71
QY 61 ACTGCCCTGTGTGCTTACTCTCTCCAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 120
DB 72 ACTGCCCTGTGTGCTTACTCTCTCCAAAGCCAGGTGAGCAACGAGGACTGCTGCAGGTG 131
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGTGACCCGCGCATCCGCGCATTTGGCCTC 180
DB 132 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGTGACCCGCGCATCCGCGCATTTGGCCTC 191
QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
DB 192 CTGACCGTCATCAGCAAGGCTGCAGC 218

RESULT 6

BM042219
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
Source

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/db_xref="taxon:9606"
/clone="IMAGE:5557096"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 100.0%; Score 207; DB 12; Length 682;
Best Local Similarity 100.0%; Pred. No. 2.8e-34;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ACTGCCCTGTGTGCTTACTCTCTCCAAAGCCAGGTGAGCAACGAGGACTGCTTGCAGGTG 120
DB 62 ACTGCCCTGTGTGCTTACTCTCTCCAAAGCCAGGTGAGCAACGAGGACTGCTTGCAGGTG 121
QY 121 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGTGACCCGCGCATCCGCGCATTTGGCCTC 180
DB 122 GAGAACTGCACCCAGCTGGGGGAGCAGTGTGTGACCCGCGCATCCGCGCATTTGGCCTC 181
QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
DB 182 CTGACCGTCATCAGCAAGGCTGCAGC 208

RESULT 7

LOCUS
DEFINITION
ACCESSION
VERSION

BG761095 60217425F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:484974 5', mRNA sequence.
BG761095
BG761095.1 GI:14071748

BM042219 682 bp mRNA linear EST 07-NOV-2001
603616172F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5557096 5', mRNA sequence.

BM042219
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTP/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L115NU354s1 row: C column: 17
High quality sequence stop: 678.

Location/Qualifiers

mRNA sequence.

ACCESSION BM750435
VERSION BM750435.1 GI:19080053
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 315)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsun@mail.kribb.re.kr
Plate: 30 row: E column: 01
High quality sequence stop: 315.

FEATURES	SOURCE
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99. <i>Other</i>	
100. <i>Other</i>	

full-length enriched cDNA library."									
ORIGIN									
Query Match	99.2%	Score	205.4	DB	12	Length	315		
Best Local Similarity	99.5%	Pred.	No. 4.5e-34						
Matches	206	Conservative	0	Mismatches	1	Indels	0	Gaps	0
QY	1	GTGACCATGAGCGTGTGCTGCTTGGCCCTGTGTGATGCAGGCTTGGCCCTGCAGCCAGGC	60						
Db	10	GTGACCATGAGCGTGTGCTTGGCCCTGTGTGATGCAGGCTTGGCCCTGCAGCCAGGC	69						
QY	61	ACTGCCCTGTGTTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCCTCAGGTG	120						
Db	70	ACTGCCCTGTGTTGCTACTCTCTGCAAAAGCCAGGTGAGCAACGAGGACTGCCTCAGGTG	129						
QY	121	GAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGGCGGCACTCCGGCAGTTGGCCTC	180						
Db	130	GAGAACTGCACCCAGCTGGGGAGCAGTGTGACCCGGCGGCACTCCGGCAGTTGGCCTC	189						
QY	181	CTGACCGCTCATCGACAAAGGCTGCAGC	207						
Db	190	CTGACCGCTCATCAGCAAGGCTGCAGC	216						

[illegible]

FEATURES	SOURCE
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100. <i>Other</i>	

full-length enriched cDNA library."					
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	Best Local Similarity	99.5%;	Pred. No. 5.6e-34;		
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Qy	1	GTGACCATGAAGCTGTGCTTGCCTCTTTGATGGCAGCGCTTGCCCTTCGACGCCAGGC	60		
Dd	10	GTGACCACGAAGCTGTGCTTGCCTCTTTGATGGCAGCGCTTGCCCTTCGACGCCAGGC	69		
Qy	61	ACTGCCCTGTGCTGCTACTCTCTCAAAAGCCCAGGTGAGCAAACGAGGACTGCCTTCAGGTG	120		
Dd	70	ACTGCCCTGTGCTGCTACTCTCTCAAAAGCCCAGGTGAGCAAACGAGGACTGCCTTCAGGTG	129		
Qy	121	GAGAACTGCACCAAGCTGGGGGACAGTGTGTGACCCGCGCGAATCCCGCAGATTGGCCTC	180		
Dd	130	GAGAATTCACCAAGCTGGGGGACAGTGTGTGACCCGCGCGAATCCCGCAGATTGGCCTC	189		
Qy	181	CTGACCGCTCATCAGCAAAAGGCTGCAGC	207		

LOCUS CB993163 851 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT13628816 NIH_MGC148 Homo sapiens cDNA clone
IMAGE:30338013 5', mRNA sequence.
ACCESSION CB993163
VERSION CB993163
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM363 row: p column: 22
High quality sequence stop: 558.
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Location/Qualifiers
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/notes="Organ: Placenta; Vector: pBluescriptR; Site: 1;
all-XhoI; Site: 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTNN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match 99.2%; Score 205.4; DB 14; Length 851;
Best Local Similarity 99.5%; Pred. No. 6.6e-34;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGACCATGAAGCTGTGCTTGCCTGTGATGGCAGGCTTGGCCCTGAGCCAGGC 60
Db |||||
78 GTGACCACGAAGGCTGTGCTTGCCTGTGATGGCAGGCTTGGCCCTGAGCCAGGC 137
QY 61 ACTGCCCTGTGCTGCTACTCTCCAAAGCCAGGTCAGCAAGGAGTGCCTGCAGGTG 120
Db |||||
138 ACTGCCCTGTGCTGCTACTCTCCAAAGCCAGGTCAGCAAGGAGTGCCTGCAGGTG 197
QY 121 GAGAACTGCACCCAGTGGGGGAGCAGTGTGTCACCGCGCGCATCCGGCAGTTGGCCTC 180
Db |||||
198 GAGAACTGCACCCAGTGGGGGAGCAGTGTGTCACCGCGCGCATCCGGCAGTTGGCCTC 257
QY 181 CTGACCGTCATCAGCAAGGCTGCAGC 207
Db |||||
258 CTGACCGTCATCAGCAAGGCTGCAGC 284

Search completed: September 18, 2004, 19:14:23
Job time : 947.591 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:35:58 ; Search time 1326.98 Seconds
(without alignments)
8655.682 Million cell updates/sec

Title: US-09-079-874-5

Perfect score: 265

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*

2: gb_htg:*

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4: gb_cm:*

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6: gb_pat:*

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8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

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34: em_htg_pln:*

35: em_htg_rdt:*

36: em_htg_mam:*

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	265	100.0	372	6	AX155553	AX155553 Sequence
2	265	100.0	946	9	HSA297436	AJ297436 Homo sapi
3	265	100.0	960	6	AR410610	AR410610 Sequence
4	265	100.0	960	6	AX201328	AX201328 Sequence
5	265	100.0	960	6	AX697426	AX697426 Sequence
6	265	100.0	960	6	BD075381	BD075381 Secretory
7	265	100.0	960	6	BD172241	BD172241 Secreted
8	265	100.0	960	6	BD172560	BD172560 Secreted
9	265	100.0	960	6	BD172879	BD172879 Secreted
10	265	100.0	960	6	BD173198	BD173198 Secreted
11	265	100.0	960	6	BD175232	BD175232 Secretory
12	265	100.0	960	9	AX358912	AX358912 Homo sapi
13	265	100.0	990	6	AX014204	AX014204 Sequence
14	265	100.0	990	6	BD205072	BD205072 Human nuc
15	265	100.0	990	9	AF043498	AF043498 Homo sapi
16	265	100.0	998	6	AR162849	AR162849 Sequence
17	265	100.0	998	6	AR302232	AR302232 Sequence
18	265	100.0	998	6	AX080304	AX080304 Sequence
19	265	100.0	998	6	BD193367	BD193367 Prostate
20	265	100.0	1015	9	BC023582	BC023582 Homo sapi
21	264.6	99.8	494	6	AR026974	AR026974 Sequence
22	263.4	99.4	369	6	BD076387	BD076387 Human pro
23	263.4	99.4	979	6	BD076397	BD076397 Human pro
24	263.4	99.4	998	6	BD264314	BD264314 PCSA: pro
25	236.2	89.1	372	6	AX155569	AX155569 Sequence
26	233	87.9	372	6	AX155567	AX155567 Sequence
27	200	75.5	157839	2	AC015718	AC015718 Homo sapi
28	198.4	74.9	100079	9	AC108002	AC108002 Homo sapi
29	198.4	74.9	103247	2	AF176678	AF176678 Homo sapi
30	198.4	74.9	105156	2	AF235094	AF235094 Homo sapi
31	195.8	73.9	286	6	AR026988	AR026988 Sequence
32	183	69.1	288	6	AR026990	AR026990 Sequence
33	169.6	64.0	373	6	AX884747	AX884747 Sequence
34	169.6	64.0	373	6	BD024357	BD024357 Sequence
35	169.6	63.6	373	6	BD076969	BD076969 5' EST of
36	134.6	50.8	441	6	AR162850	AR162850 Sequence
37	134.6	50.8	441	6	AR302233	AR302233 Sequence
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39	134.6	50.8	441	6	BD193368	BD193368 Prostate
40	134.6	50.8	864	10	AF319173	AF319173 Mus muscu
41	124	46.8	758	6	AX014148	AX014148 Sequence
42	124	46.8	758	6	BD205056	BD205056 Human nuc
43	119.4	45.1	441	6	BD264315	BD264315 PCSA: pro
44	118.4	44.7	232	6	AR026992	AR026992 Sequence
45	107.2	40.5	190653	10	AC118022	AC118022 Mus muscu

ALIGNMENTS

RESULT 1
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LOCUS AX155553 Sequence 2 from Patent WO0140309. 372 bp DNA linear PAT 22-JUN-2001
DEFINITION AX155553
ACCESSION AX155553
VERSION AX155553.1 GI:14536783
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Devaux,B., Keller,G.A., Koeppen,H. and Lasky,L.A.
TITLE Anti-prostate stem cell antigen (psca) antibody compositions and methods of use

JOURNAL		Patent: WO 0140309-A 2 07-JUN-2001;	
Genentech, Inc. (US)		Location/Qualifiers	
FEATURES		1..372	
source		/organism="Homo sapiens"	
		/mol_type="unassigned DNA"	
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Query Match		100.0%; Score 265; DB 6; Length 372;	
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QY	1	CGAGGACTGCTGAGTGGAGAACTGCACCCAGCTGGGGAGAGCACTGCTGGACCGCGG	60
Db	96	CGAGGACTGCTGAGTGGAGAACTGCACCCAGCTGGGGAGAGCACTGCTGGACCGCGG	155
QY	61	CATCCGCGCAGTTGGCTCTCTGACCGTCAATCAGCAAGAGCTGACGTTGAACTGGTGA	120
Db	156	CATCCGCGCAGTTGGCTCTCTGACCGTCAATCAGCAAGAGCTGACGTTGAACTGGTGA	215
QY	121	TGACTCAGAGGACTACTAGCTGGGCAAGAGCAATCAGCTGCTGTGACACCGACTTGTG	180
Db	216	TGACTCAGAGGACTACTAGCTGGGCAAGAGCAATCAGCTGCTGTGACACCGACTTGTG	275
QY	181	CAACGCCAGCGGGGCCCATGCCCTGCAGCCGCTGCCGCCATCTCTTGGCTGCTCCCTGC	240
Db	276	CAACGCCAGCGGGGCCCATGCCCTGCAGCCGCTGCCGCCATCTCTTGGCTGCTCCCTGC	335
QY	241	ACTCGGCTGCTGCTCTGGGACCC	265
Db	336	ACTCGGCTGCTGCTCTGGGACCC	360
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LOCUS		Homo sapiens mRNA for prostate stem cell antigen (PSCA gene).	
DEFINITION		AJ297436	
ACCESSION		AJ297436.1 GI:9367211	
VERSION		prostate stem cell antigen; PSCA gene.	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Bahrenberg,G., Brauers,A., Joost,H.G. and Jakse,G.	
TITLE		Reduced expression of PSCA, a member of the LY-6 family of cell surface antigens, in bladder, esophagus, and stomach tumors	
JOURNAL		Biochem. Biophys. Res. Commun. 275 (3), 783-788 (2000)	
MEDLINE		20431743	
PUBMED		10973799	
REFERENCE		2 (bases 1 to 946)	
AUTHORS		Bahrenberg,G.	
TITLE		Direct Submission	
JOURNAL		Submitted (12-JUL-2000) Bahrenberg G., Institut fuer Pharmakologie und Toxikologie, RWTH Aachen, Wendingweg2, Aachen, NRW, 52057, GERMANY	
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QY	61	CATCCGCGCAGTTGGCTCTCTGACCGTCAATCAGCAAGAGCTGACGTTGAACTGGTGA	120
Db	175	CATCCGCGCAGTTGGCTCTCTGACCGTCAATCAGCAAGAGCTGACGTTGAACTGGTGA	234
QY	121	TGACTCAGAGGACTACTAGCTGGGCAAGAGCAATCAGCTGCTGTGACACCGACTTGTG	180
Db	235	TGACTCAGAGGACTACTAGCTGGGCAAGAGCAATCAGCTGCTGTGACACCGACTTGTG	294
QY	181	CAACGCCAGCGGGGCCCATGCCCTGCAGCCGCTGCCGCCATCTCTTGGCTGCTCCCTGC	240
Db	295	CAACGCCAGCGGGGCCCATGCCCTGCAGCCGCTGCCGCCATCTCTTGGCTGCTCCCTGC	354
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RESULT 3		AR410610	
LOCUS		960 bp DNA linear PAT 18-DEC-2003	
DEFINITION		Sequence 17 from patent US 6635468.	
ACCESSION		AR410610	
VERSION		AR410610.1 GI:40162110	
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 960)	
AUTHORS		Ashkenazi,A., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.B., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.	
TITLE		Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL		Patent: US 6635468-A 17 21-OCT-2003;	
FEATURES		Location/Qualifiers	
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		/mol_type="genomic DNA"	
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Best Local Similarity		100.0%; Pred. No. 4.7e-43;	
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QY	61	CATCCGCGCAGTTGGCTCTCTGACCGTCAATCAGCAAGAGCTGACGTTGAACTGGTGA	120
Db	145	CATCCGCGCAGTTGGCTCTCTGACCGTCAATCAGCAAGAGCTGACGTTGAACTGGTGA	204

QY	121	TGACTCAGAGACTACTACTACGTGGGCAAGAAGACATCAGTCTGTGACACCGACTTGTG	180			
DB	205	TGACTCAGAGACTACTACTACGTGGGCAAGAAGACATCAGTCTGTGACACCGACTTGTG	264			
QY	181	CAACGCCACAGCGGGGCCCATGCTCCCTGTCAGCGCGGTGCGGCATCTTGGCGTGTCTCCCTGC	240			
DB	265	CAACGCCACAGCGGGGCCCATGCTCCCTGTCAGCGCGGTGCGGCATCTTGGCGTGTCTCCCTGC	324			
QY	241	ACTCGGCTGTCTGTGGGGACCC	265			
DB	325	ACTCGGCTGTCTGTGGGGACCC	349			
RESULT 4						
LOCUS	AX201328	960 bp	DNA linear PAT 30-AUG-2001			
DEFINITION	Sequence 7 from Patent WO0153486.					
ACCESSION	AX201328					
VERSION	AX201328.1	GI:15391156				
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	1					
AUTHORS	Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,					
	Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,					
	Stone,D.M., Watanabe,C.K. and Wood,W.I.					
TITLE	Compositions and methods for the treatment of tumour					
JOURNAL	Patent: WO 0153486-A 7 26-JUL-2001;					
FEATURES	Genentech, Inc. (US)					
	Location/Qualifiers					
	source	1..960				
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Query Match 100.0%; Score 265; DB 6; Length 960;						
Best Local Similarity 100.0%; Pred. No. 4.7e-43;						
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0						
QY	1	CGAGGACTGCTCGAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCG	60			
DB	85	CGAGGACTGCTCGAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGCG	144			
QY	61	CATCCGCGAGTTGGCTCTTGACCGTCATCAGCAAGGCTGAGCTTGAACCTGCTGGA	120			
DB	145	CATCCGCGAGTTGGCTCTTGACCGTCATCAGCAAGGCTGAGCTTGAACCTGCTGGA	204			
QY	121	TGACTCAGAGGACTACTACGTGGGCAAGAAGAAATCACGTGTGTGACACCGACTTGTG	180			
DB	205	TGACTCAGAGGACTACTACGTGGGCAAGAAGAAATCACGTGTGTGACACCGACTTGTG	264			
QY	181	CAACGCCACAGCGGGGCCCATGCGCTGACGCGGCTGCGGCATCTTGGCGTGTCTCCCTGC	240			
DB	265	CAACGCCACAGCGGGGCCCATGCGCTGACGCGGCTGCGGCATCTTGGCGTGTCTCCCTGC	324			
QY	241	ACTCGGCTGTCTGTGGGGACCC	265			
DB	325	ACTCGGCTGTCTGTGGGGACCC	349			
RESULT 5						
LOCUS	AX697426	960 bp	DNA linear PAT 02-APR-2000			
DEFINITION	Sequence 17 from Patent WO0104311.					
ACCESSION	AX697426					
VERSION	AX697426.1	GI:29498554				
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Ashkenazi,A.J., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0104311-A 17 18-JAN-2001;
FEATURES	Genentech Inc. (US)
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VERSION	JP 2001516580-A/14.
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REFERENCE	1 (bases 1 to 960)
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding the same
JOURNAL	Patent: JP 2001516580-A 14 02-OCT-2001;
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 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI
 JEAN CHEN,
 PI JEAN YUAN
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 encoding the same
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 FT /organism='Homo sapiens (human)'.
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 Best Local Similarity 100.0%; Pred. No. 4.7e-43;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 VERSION
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 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 960)
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 YUAN,J.
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 PN JP 200223786-A/14
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 encoding the same
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 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGGACCGCGG 60
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
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JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC
(C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC Secreted
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same
FH Key Location/Qualifiers
PI source 1..960
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QY 1 CGAGGACTCCCTGCAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCG 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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1 (bases 1 to 960)
AUTHORS
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE
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the same
JOURNAL
Patent: JP 2002238588-A 14 27-AUG-2002;
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OS Homo sapiens (human)
COMMENT
PN JP 2002238588-A/14

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QY 1 CGAGGACTCCCTGCAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCG 60
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DEFINITION	Secretory and transmembrane polypeptide and nucleic acid encoding the same.				
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.				
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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 960) Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagte, A., Vandlen, R., Watanabe, C., Weiland, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P. The Secretd Protein Discovery Initiative (SPDI), a large-scale effort to identify Novel Human Secretd and Transmembrane Proteins: A Bioinformatics Assessment Genome Res. 13 (10), 2265-2270 (2003) 12975309				
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)				
PUBMED	12975309				
REFERENCE	2 (bases 1 to 960) Clark, H.F. Direct Submission Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA				
TITLE	Location/Qualifiers				
JOURNAL	1..960 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DNA34435" 1..960 /locus_tag="UNQ206" 1..361 /locus_tag="UNQ206" /note="PRO232" /codon_start=2 /product="prostate stem cell A" /protein_id="AAQ89271.1" /db_xref="GI:37182942" /translation="ELALLMAGLALQGTALLCYSCAKVSNEDCLQVENCITQIGROCIWTARIVAGLITVISKGSCNLCVDSQDYVVGKNIITCCDTDLGNAGAHALQPAALAILLALPALLLWPGQL"				
FEATURES	source				
gene					
CDS					
ORIGIN					

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DB	85	CGAGGACTGCTGCTGAGTGGAGAACTGACCCAGCTGGGGAGCAGTGGTGGACCGCGC	144
QY	61	CATCCGGCGAGTTGGCCCTCTGACCGGTATCAGCAAAAGGTGACAGTGAACCTGCGTGA	120
DB	145	CATCCGGCGAGTTGGCCCTCTGACCGGTATCAGCAAAAGGTGACAGTGAACCTGCGTGA	204
QY	121	TGACTCAGAGGACTACTACGTGGGCAAGAGAACATCAGTGTGTGACACCGACTTGTG	180
DB	205	TGACTCAGAGGACTACTACGTGGGCAAGAGAACATCAGTGTGTGACACCGACTTGTG	264
QY	181	CAAGCCAGCGGGGCCCATGCTCCCTGAGCGCGGTGCGGCCATCTTCCGTGTCTCCCTGC	240
DB	265	CAAGCCAGCGGGGCCCATGCTCCCTGAGCGCGGTGCGGCCATCTTCCGTGTCTCCCTGC	324
QY	241	ACTCGGCTGCTGCTCTGGGGACCC	265
DB	325	ACTCGGCTGCTGCTCTGGGGACCC	349
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LOCUS	Homo sapiens clone DNA34435 prostate stem cell A (UNQ206) mRNA,		
DEFINITION	partial cds.		
ACCESSION	AY358912		
VERSION	AY358912.1 GI:37182941		
KEYWORDS	P11_CDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 960) Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wleand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.		
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment		
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)		
PUBMED	12975309		
REFERENCE	2 (bases 1 to 960)		
AUTHORS	Clark, H.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
FEATURES	Location/Qualifiers		
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gene			
CDS			
ORIGIN			

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 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTGAGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGG 60
 DB 85 CGAGGACTGCTGAGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGG 144
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 QY 121 TGACTCAGAGACTACTAGTGGGCAAGAGACATCAGTGTGTGACCGACTTGTG 180
 DB 205 TGACTCAGAGACTACTAGTGGGCAAGAGACATCAGTGTGTGACCGACTTGTG 264
 QY 181 CAAGCGCAGCGGGCCCATGCTGACCGGCTGCGCGCATCTTGGCTGCTCCCTGC 240
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 QY 241 ACTCGGCTGCTGCTGCGGAGCC 265
 DB 325 ACTCGGCTGCTGCTGCGGAGCC 349

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 LOCUS AX014204 990 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 108 from Patent WO954447.
 ACCESSION AX014204
 VERSION AX014204.1 GI:10040611
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
 Pilarsky,C.
 Human nucleic acid sequences of bladder tumour tissue
 Patent: WO 954447-A 108 28-OCT-1999;
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
 BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUEH GENOMFORSCHUN
 (DE); PILARSKY CHRISTIAN (DE)

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 DB 113 CGAGGACTGCTGAGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGG 172
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 QY 181 CAAGCGCAGCGGGCCCATGCTGACCGGCTGCGCGCATCTTGGCTGCTCCCTGC 240
 DB 293 CAAGCGCAGCGGGCCCATGCTGACCGGCTGCGCGCATCTTGGCTGCTCCCTGC 352
 QY 241 ACTCGGCTGCTGCTGCGGAGCC 265

DB 353 ACTCGGCTGCTGCTGCGGAGCC 377

RESULT 14
 BD205072
 LOCUS BD205072 990 bp DNA linear PAT 17-JUL-2003
 DEFINITION Human nucleic acid sequence originating in cystic cancer tissue.
 ACCESSION BD205072
 VERSION BD205072.1 GI:33014842
 KEYWORDS JP 2002512023-A/26
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and
 Rosenthal,A.

Human nucleic acid sequence originating in cystic cancer tissue
 Patent: JP 2002512023-A 26 23-APR-2002;
 METAGEN GESELLSCHAFT FUEH GENOM FORSCHUNG MBH
 OS Homo sapiens (human)
 PN JP 2002512023-A/26
 PD 23-APR-2002
 PF 15-APR-1999 JP 2000544779
 PR 21-APR-1998 DE 198 18 619,3
 PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
 PI EDGAR DAHL,
 PI ANDRE ROSENTHAL
 PI PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P13/10,
 PC A61P35/00,
 PC C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12P21/08, C12Q1/68, PC
 C12N15/00,
 PC A61K37/02, C12N5/00
 CC Human nucleic acid sequence originating in cystic cancer CC

PH Key

FT source

1..990

Location/Qualifiers

/organism="Homo sapiens (human)"

FEATURES

source

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Location/Qualifiers

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Query Match 100.0%; Score 265; DB 6; Length 990;
 Best Local Similarity 100.0%; Pred. No. 4.7e-43;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTGAGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGG 60
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 QY 61 CATCGGCGAGTGGGCTCTGCTGAGCGTATCAGCAAGGCTGAGCTTGAACCTGGTGA 120
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 QY 121 TGACTCAGAGACTACTAGTGGGCAAGAGACATCAGTGTGTGACCGACTTGTG 180
 DB 233 TGACTCAGAGACTACTAGTGGGCAAGAGACATCAGTGTGTGACCGACTTGTG 292
 QY 181 CAAGCGCAGCGGGCCCATGCTGACCGGCTGCGCGCATCTTGGCTGCTCCCTGC 240
 DB 293 CAAGCGCAGCGGGCCCATGCTGACCGGCTGCGCGCATCTTGGCTGCTCCCTGC 352
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 DB 353 ACTCGGCTGCTGCTGCGGAGCC 377

RESULT 15
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LOCUS AF043498 990 bp mRNA linear PRI 24-FEB-1998
 DEFINITION Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds.
 ACCESSION AF043498
 VERSION AF043498.1 GI:2909843
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 990)
 AUTHORS Reiter, R.E., Gu, Z., Watabe, T., Thomas, G., King, S., Davis, E., Wahl, M., Nisitani, S., Yamashiro, J., Le Beau, M.M., Losa, M. and Witte, O.N.
 TITLE Prostate stem cell antigen: a cell surface marker overexpressed in prostate cancer
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (4), 1735-1740 (1998)
 MEDLINE 98132661
 PUBMED 9465086
 REFERENCE 2 (bases 1 to 990)
 AUTHORS Reiter, R.E.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-1998) Urology, UCLA, 66-134 CHS 10833 Le Conte Ave., Los Angeles, CA 90095, USA
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Query Match 100.0%; Score 265; DB 9; Length 990;
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QY	1	CGAGGACTGCTGCAGTGGAGAACCTGCACCCAGCTGGGGAGCAGTGTGACCGCGC	60
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QY	61	CATCCGCGAGTGGCTCTGACCGTCATCAGCAAGGCTCAGCTTGAACCTGCGTGA	120
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QY	121	TGACTCAGAGGACTACTAGCTGGGCAAGAAGAACATCAGTCTGTGACACCGACTTGT	180
Db	233	TGACTCAGAGGACTACTAGCTGGGCAAGAAGAACATCAGTCTGTGACACCGACTTGT	292
QY	181	CAACGCCAGGGGGCCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC	240
Db	293	CAACGCCAGGGGGCCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC	352
QY	241	ACTCGGCTGCTGCTCTGGGGACCC	265
Db	353	ACTCGGCTGCTGCTCTGGGGACCC	377

Search completed: September 18, 2004, 13:27:07
 Job time : 1326.98 secs

Pump
Sheet

CC and polypeptides are useful for detecting, diagnosing, monitoring,
 CC staging, prognosticating, in vivo imaging, preventing, treating or
 CC determining the predisposition of a subject to diseases and conditions of
 CC the urinary tract, such as urinary tract cancer. Antibodies specifically
 CC binding to an epitope of Ustil antigen, and agonists are useful for
 CC treating urinary tract diseases, tumours and metastases
 XX
 SQ Sequence 265 BP; 48 A; 89 C; 83 G; 45 T; 0 U; 0 Other;

Query Match 100.0%; Score 265; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 9.4e-57;
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 QY 121 TGACTCACAGGACTACTACGTGGCAAGAAACATCAGTCTGTGACCCGACTTTGT 180
 Db 121 TGACTCACAGGACTACTACGTGGCAAGAAACATCAGTCTGTGACCCGACTTTGT 180
 QY 181 CAACGCGACGGGGCCCATCGCTGAGCGCGCTCGCGCATCTTGGCTGCTCCCTGC 240
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 QY 241 ACTCGGCTGCTGCTCTGGGGACCC 265
 Db 241 ACTCGGCTGCTGCTCTGGGGACCC 265

RESULT 2
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 ID AAV68607 standard; cDNA; 265 BP.
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 AC AAV68607;
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 XX
 DT 16-MAR-1999 (first entry)
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 DE Human PS116 EST clone 1863905.
 XX
 KW Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 KW detection; therapy; prostate cancer; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9851805-A1.
 PN
 PD 19-NOV-1998.
 XX
 PF 15-MAY-1998; 98WO-US010041.
 XX
 PR 15-MAY-1997; 97US-00856653.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman FN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD;
 XX
 DR WPI; 1999-045234/04.
 XX
 PT New method for detecting diseases of the prostate - comprises use of a
 PT PS116 polynucleotide, protein or antibodies, useful for preventing and
 PT treating prostate infections and cancer.
 XX
 PS Claim 1; Page 92; 118pp; English.
 XX
 CC This sequence represents an expressed sequence tag (EST) clone of the
 CC PS116 gene isolated from a human prostate tissue library. This sequence

CC can be used in the method of the invention for detecting a target PS116
 CC polynucleotide (PN), that comprises: contacting a sample with at least 1
 CC PS116-specific PN or complement; and detecting the target PS116 PN, where
 CC the specific PN has at least 50% identity with this sequence. The PNs,
 CC PS116 polypeptides or PS116 amplicons are used to detect prostate
 CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
 CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
 CC solid phase. The polypeptides are used for detecting PS116-specific Abs
 CC in a sample, and for producing Abs after immunising a subject. Plasmids
 CC encoding PS116 epitopes can also be administered to a subject to obtain
 CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
 CC staging, monitoring, prognosticating, in vivo imaging, preventing, and
 CC treating or determining the predisposition of a subject to diseases and
 CC conditions of the prostate, such as prostate cancer. The Abs and agonists
 CC or inhibitors are useful for treating prostate diseases, tumours and
 CC metastases
 XX

SQ Sequence 265 BP; 48 A; 89 C; 83 G; 45 T; 0 U; 0 Other;

Query Match 100.0%; Score 265; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 9.4e-57;
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 QY 1 CGAGGACTCCCTCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 60
 Db 1 CGAGGACTCCCTCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 60
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 Db 61 CATCCGCGAGTGGCTCTCAGCTCATCAGCAAGGCTGCAGCTTGAACCTGGTGA 120
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 QY 241 ACTCGGCTGCTGCTCTGGGGACCC 265
 Db 241 ACTCGGCTGCTGCTCTGGGGACCC 265

RESULT 3
 AAD08171
 ID AAD08171 standard; cDNA; 372 BP.
 XX
 AC AAD08171;
 XX
 DT 07-AUG-2001 (first entry)
 XX
 DE Human prostate stem cell antigen (PSCA) cDNA.
 XX
 KW Human; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
 KW Glycoprotein; cancer; prostate; bladder; lung; tumour; ss.
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 OS Homo sapiens.
 XX
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 FT mat_peptide 61..372
 FT /*tag= c
 FT /product= "Mature human PSCA protein"
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 XX WO200140309-A2.
 XX
 XX 07-JUN-2001.
 XX

PF 27-OCT-2000; 2000WO-US029603.
XX
PR 29-OCT-1999; 99US-0162558P.
PR 16-FEB-2000; 2000US-0182872P.
XX
PA (GETH) GENENTECH INC.
XX
PI Devaux B, Keller G, Koeppen H, Lasky LA;
XX WPI; 2001-389954/41.
DR P-PSDB; AAE03746.
XX
XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
PT on binding to PSCA on mammalian cell and inhibits growth of PSCA-
PT expressing cancer cells in vivo, useful for killing PSCA-expressing
PT cancer cells.
XX
XX Example 1; Page 99; 112pp; English.
XX
XX The present sequence is a cDNA encoding human prostate stem cell antigen
CC (PSCA). PSCA is a single subunit glycoprotein that is expressed on the
CC cell surface as a glycosylphosphatidylinositol (GPI)-anchored protein.
CC The present invention relates to anti-PSCA antibody composition and
CC methods of killing PSCA-expressing cancer cells. PSCA is useful for
CC inhibiting and killing the growth of PSCA-expressing cancer cells such as
CC prostate cancer, bladder cancer or lung cancer cells. Humanised antibody
CC conjugated to a toxin or a radioactive isotope is used for killing the
CC cancer cells. PSCA is useful for specifically targeting PSCA-expressing
CC tumour cells in vivo and for inhibiting or killing these cells. The
CC antibodies are also useful for treating the above mentioned cancers and
CC for diagnosing and staging of PSCA-expressing cancer, for purification or
CC immunoprecipitation of PSCA from cells, and for detection and
CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating
CC cancers by gene therapy techniques
XX
SQ Sequence 372 BP; 67 A; 121 C; 116 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 265; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 96 CGAGGACTGCTGCAGTGGAGAACTGACCCAGCTGGGGGAGCAGTGTGGACCGCGG 155

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Qy 121 TGACTCAGGACTACTACTGTTGGCAAGAAAGACATCATGCTGTGACACCGACTTGTG 180
Db 216 TGACTCAGGACTACTACTGTTGGCAAGAAAGACATCATGCTGTGACACCGACTTGTG 275

Qy 181 CAACGCCAGGGGGCCATCCCTGACGGCGCTGCGCCATCTTTGCGTGTGCTCCCTGC 240
Db 276 CAACGCCAGGGGGCCATCCCTGACGGCGCTGCGCCATCTTTGCGTGTGCTCCCTGC 335

Qy 241 ACTCGGCTGTGCTGTGGGACCC 265
Db 336 ACTCGGCTGTGCTGTGGGACCC 360

RESULT 4
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XX
XX AAX52217;
XX
XX 25-JUN-1999 (first entry)
DT
XX Protein PRO232 cDNA clone DNA34435-1140.
DE
XX Secreted protein; transmembrane protein; human; enterocolitis;
KW

KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
KW wound healing; tissue repair; ss.
XX
OS Homo sapiens.
XX
PN W09914328-A2.
XX
XX 25-MAR-1999.
PD
XX
XX 16-SEP-1998; 98WO-US019330.
PF 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
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PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
XX
XX (GETH) GENENTECH INC.
XX
XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
PI WPI; 1999-229533/19.
XX P-PSDB; AAY13347.
DR
XX

PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration.
 XX
 PS Claim 2; Fig 8; 320pp; English.
 XX
 CC AAX52213-74 encode secreted and transmembrane human proteins, and are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides have
 CC specific uses based on their homology to known polypeptides, e.g. PRO211
 CC and PRO217 can be used for disorders associated with the preservation and
 CC maintenance of gastrointestinal mucosa and the repair of acute and
 CC chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,
 CC gastrointestinal ulceration and congenital microvillus atrophy), skin
 CC diseases associated with abnormal keratinocyte differentiation (e.g.
 CC psoriasis, epithelial cancers such as lung squamous cell carcinoma of the
 CC vulva and gliomas), potent effects on cell growth and development,
 CC diseases related to growth or survival of nerve cells including
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.
 CC PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX
 SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;
 Query Match 100.0%; Score 265; DB 2; Length 960;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAGGACTGCTGAGTGGAGAACTGCACCGCTGGGGAGCAGTGTGACCGCGG 60
 DB 85 CGAGGACTGCTGAGTGGAGAACTGCACCGCTGGGGAGCAGTGTGACCGCGG 144
 QY 61 CATCCGCGAGTGGCTCTCCTGACCGTATCAGCAAGGCTGAGTGTGACCGTGTGA 120
 DB 145 CATCCGCGAGTGGCTCTCCTGACCGTATCAGCAAGGCTGAGTGTGACCGTGTGA 204
 QY 121 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTGTGACACCGACTTGTG 180
 DB 205 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTGTGACACCGACTTGTG 264
 QY 181 CAACGCGAGCGGGCCCATGCCCTGACGGCTGCGGCATCCTTGGCTGCTCCCTGC 240
 DB 265 CAACGCGAGCGGGCCCATGCCCTGACGGCTGCGGCATCCTTGGCTGCTCCCTGC 324
 QY 241 ACTCGGCTGCTGCTCTGGGGACCC 265
 DB 325 ACTCGGCTGCTGCTCTGGGGACCC 349
 RESULT 5
 AD78337
 ID ADC78337 standard; cDNA; 960 BP.
 XX
 AC ADC78337;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human PRO232 cDNA.
 XX
 KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;

KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
 XX Homo sapiens.
 XX WO200015796-A2.
 PN 23-MAR-2000.
 PD 15-SEP-1999; 99WO-US021090.
 XX 16-SEP-1998; 98WO-US019330.
 PR (GETH) GENENTECH INC.
 PA Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 PI Yuan J;
 XX WPI; 2000-271434/23.
 DR P-PSDB; ADC78338.
 XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX Claim 2; SEQ ID NO 17; 355pp; English.
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or
 CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the human
 CC PRO cDNA of the invention.
 XX
 SQ Sequence 960 BP; 182 A; 327 C; 274 G; 177 T; 0 U; 0 Other;
 Query Match 100.0%; Score 265; DB 3; Length 960;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAGGACTGCTGAGTGGAGAACTGCACCGCTGGGGAGCAGTGTGACCGCGG 60
 DB 85 CGAGGACTGCTGAGTGGAGAACTGCACCGCTGGGGAGCAGTGTGACCGCGG 144
 QY 61 CATCCGCGAGTGGCTCTCCTGACCGTATCAGCAAGGCTGAGTGTGACCGTGTGA 120
 DB 145 CATCCGCGAGTGGCTCTCCTGACCGTATCAGCAAGGCTGAGTGTGACCGTGTGA 204
 QY 121 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTGTGACACCGACTTGTG 180
 DB 205 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTGTGACACCGACTTGTG 264
 QY 181 CAACGCGAGCGGGCCCATGCCCTGACGGCTGCGGCATCCTTGGCTGCTCCCTGC 240
 DB 265 CAACGCGAGCGGGCCCATGCCCTGACGGCTGCGGCATCCTTGGCTGCTCCCTGC 324
 QY 241 ACTCGGCTGCTGCTCTGGGGACCC 265
 DB 325 ACTCGGCTGCTGCTCTGGGGACCC 349
 RESULT 6
 AAF72375
 ID AAF72375 standard; cDNA; 960 BP.
 XX
 AC AAF72375;
 XX
 DT 24-APR-2001 (first entry)
 XX

DE Human PRO232 cDNA.
XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; antitropic; antiaschmatic; antirheumatic; cancer;
KW antiarthritic; antiferility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; expressed sequence tag; EST; ss.
XX
OS Homo sapiens.
XX
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
XX 22-FEB-2000; 2000WO-US004414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145588P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavini IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-081051/09.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX
XX Claim 2; Fig 8; 393pp; English.
XX
XX The present sequence is an EST used to isolate one of sixty one nucleic
CC acids encoding novel secreted and transmembrane PRO polypeptides. The PRO
CC polypeptides are useful for treating skin diseases (e.g. psoriasis),
CC cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders
CC (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), wound repair, cardiovascular disorders
CC (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes
CC and retinal disorders such as retinitis pigmentosa. The PRO nucleic
CC acids have applications in molecular biology, including use as
CC hybridization probes, and in chromosome and gene mapping
XX
SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 265; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGCTGGGGAGCAGTCTGTCACCGCGG 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
85 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGCTGGGGAGCAGTCTGTCACCGCGG 144

QY 61 CATCGCGCACTTGGCCTCCTGACCGTCATCAGCAAAAGGCTGCAGCTTGAACCTGGTGA 120
DB 145 CATCGCGCACTTGGCCTCCTGACCGTCATCAGCAAAAGGCTGCAGCTTGAACCTGGTGA 204
QY 121 TGAATCAGAGCACTACTACGTGGGCAAGAAACATCACGTGCTGTGACACCGACTTGTG 180
DB 205 TGACTCAGAGCACTACTACGTGGGCAAGAAACATCACGTGCTGTGACACCGACTTGTG 264
QY 181 CAAGCCAGCGGGGCCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 240
DB 265 CAAGCCAGCGGGGCCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 324
QY 241 ACTCGGCTGCTGCTGCTGGGGACCC 265
DB 325 ACTCGGCTGCTGCTGCTGGGGACCC 349

RESULT 7
ABK40257
ID ABK40257 standard; cDNA; 960 BP.
XX
AC ABK40257;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO232 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US003565.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
XX WPI; 2002-205567/26.
DR P-PSDB; AAU86131.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
PS Claim 50; Fig 7; 302pp; English.

PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 03-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Feng S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini J;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 XX WPI; 2003-329602/31.
 DR P-PSDB; AB071894.
 XX
 XX New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, in generating probes and in tissue typing.
 XX
 XX Claim 2; Fig 8; 484pp; English.
 XX
 CC The invention relates to an isolated nucleic acid with at least 80%
 CC nucleic acid sequence identity to a nucleotide sequence encoding one of
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 CC PRO protein extracellular domain. Also included are a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
 CC polypeptide (by culturing the host cell for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),
 CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
 CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
 CC number (detailed in the specification); or (c) an extracellular domain of
 CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
 CC peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a
 CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
 CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
 CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
 CC modulating at least one biological activity of a cell expressing a PRO245
 CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
 CC transgenic animals or knock-out animals which may be used in the
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy, in chromosome identification, as
 CC chromosome markers, or in generating probes. The PRO polypeptides are
 CC useful as molecular markers for protein electrophoresis, and the isolated
 CC nucleic acids may be used for recombinantly expressing those markers. The
 CC PRO polypeptides and nucleic acids may also be used in tissue typing.
 CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. The present sequence encodes a PRO protein
 XX
 XX Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 265; DB 7; Length 960;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-56;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAGGACTGCTGCTGAGGTGGAGAACTGACCCAGCTGGGGAGCAGTCTGGACCGCGG 60
 DB 85 CGAGGACTGCTGCTGAGGTGGAGAACTGACCCAGCTGGGGAGCAGTCTGGACCGCGG 144
 QY 61 CATCGGCGCAGTTGGCTCTGACCGTCATCAGCAAAAGGCTGACGCTTGAATCGCTGGA 120
 DB 145 CATCGGCGCAGTTGGCTCTGACCGTCATCAGCAAAAGGCTGACGCTTGAATCGCTGGA 204
 QY 121 TGACTCAGGACTACTACGTGGGCAAGAAATCAGCTGCTGTGACACCGACTTTGTG 180
 DB 205 TGACTCAGGACTACTACGTGGGCAAGAAATCAGCTGCTGTGACACCGACTTTGTG 264
 QY 181 CAAGCCAGCGGGCCCATGCTGAGCGCGGCTGCCGCCATCCTTGGCTGTCTCCCTGC 240
 DB 265 CAAGCCAGCGGGCCCATGCTGAGCGCGGCTGCCGCCATCCTTGGCTGTCTCCCTGC 324
 QY 241 ACTGGGCTGCTGCTCTGGGGACCC 265
 DB 325 ACTGGGCTGCTGCTCTGGGGACCC 349
 XX
 XX RESULT 11
 XX ACD07413
 XX ID ACD07413 standard; cDNA; 960 BP.
 XX AC ACD07413;
 XX XX
 XX DT 07-AUG-2003 (first entry)
 XX
 XX DE Novel human secreted and transmembrane protein PRO232 cDNA.
 XX
 XX KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
 KW diagnostic; biosensor; bioindicator; Parkinson's disease;
 KW Alzheimer's disease; inflammation; nephritis; wound healing;
 KW nerve repair; collateral blood vessel formation; cancer;
 KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
 KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
 KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
 KW infertility; gene therapy; gene; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN US2002197671-A1.
 XX
 XX PD 26-DEC-2002.
 XX
 XX PF 17-JUL-2001; 2001US-00907824.
 XX
 XX PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 28-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 31-OCT-1997; 97US-0064248P.
 PR 03-NOV-1997; 97US-0064809P.
 PR 07-NOV-1997; 97US-0065186P.
 PR 12-NOV-1997; 97US-0065846P.
 PR 17-NOV-1997; 97US-0065893P.
 PR 18-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 98WO-US025594.
 PR 13-SEP-1999; 98WO-US025944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 01-DEC-1999; 98WO-US028301.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.
 PR 20-DEC-1999; 98WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 PA (GETH) GENENTECH INC.
 PI Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IU;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI; 2003-370793/35.
 DR P-PSDB; ABO01777.
 DR
 XX New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
 XX PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
 PT

PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
 PT or strokes.
 XX Claim 2; Fig 8; 482pp; English.
 XX
 CC The invention describes a new isolated nucleic acid molecule comprising
 CC the full length coding sequence of the DNA deposited with the American
 CC Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence
 CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising
 CC any of 61 sequences having 164-1119 amino acids fully defined in the
 CC specification. The PRO polypeptides or polynucleotides are useful as
 CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting or treating e.g. Parkinson's disease,
 CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve
 CC repair, collateral blood vessel formation, cancers (e.g. colorectal
 CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
 CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
 CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring), or
 CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
 CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
 CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
 CC therapeutic intervention in these diseases, and diagnostic determination
 CC of the presence of these diseases. The PRO polypeptides are also useful
 CC as molecular weight markers, or for chromosome identification. The PRO
 CC genes are useful as hybridisation probes, or for screening libraries of
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. This sequence
 CC encodes a novel human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;
 Query Match 100.0%; Score 265; DB 7; Length 960;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCGCGCG 60
 Db 85 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGACCGCGCG 144
 QY 61 CATCCGCGCAGTTGGCTCTCTGACCTCATCAACAAAGCTGCAGTTGAATGCGTGA 120
 Db 145 CATCCGCGCAGTTGGCTCTCTGACCTCATCAACAAAGCTGCAGTTGAATGCGTGA 204
 QY 121 TGACTACAGGACTACTACGTGGGCAAGAGACATCAGTGTGTGACACCGACTGTG 180
 Db 205 TGACTACAGGACTACTACGTGGGCAAGAGACATCAGTGTGTGACACCGACTGTG 264
 QY 181 CAACGCCAGCGGGGCCCATGCCCTGCAGCGGCTGCCCATCTTGGCTGCTCCCTGC 240
 Db 265 CAACGCCAGCGGGGCCCATGCCCTGCAGCGGCTGCCCATCTTGGCTGCTCCCTGC 324
 QY 241 ACTCGGCTGCTGCTGTGGGGACCC 265
 Db 325 ACTCGGCTGCTGCTGTGGGGACCC 349
 RESULT 12
 ABX71461
 ID ABX71461 standard; cDNA; 960 BP.
 XX
 XX ABX71461;
 XX
 DT 10-MAR-2003 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO232.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
 KW gastrointestinal ulceration; skin disease; ss; gene;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; inflammatory disease;
 KW rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
 KW atherosclerosis; cardiac injury; infertility; birth defect;

KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
 KW diabetic complication; wound repair.

XX Homo sapiens.

XX US2002132240-A1.

XX PD 19-SEP-2002.

XX PF 18-JUL-2001; 2001US-00909320.

XX PR 17-SEP-1997; 97US-0059113P.

XX PR 17-SEP-1997; 97US-0059115P.

XX PR 17-SEP-1997; 97US-0059117P.

XX PR 17-SEP-1997; 97US-0059121P.

XX PR 17-SEP-1997; 97US-0059122P.

XX PR 17-SEP-1997; 97US-0059184P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 15-OCT-1997; 97US-0062125P.

XX PR 17-OCT-1997; 97US-0062285P.

XX PR 17-OCT-1997; 97US-0062287P.

XX PR 21-OCT-1997; 97US-0063486P.

XX PR 24-OCT-1997; 97US-0062814P.

XX PR 24-OCT-1997; 97US-0062816P.

XX PR 24-OCT-1997; 97US-0063045P.

XX PR 24-OCT-1997; 97US-0063120P.

XX PR 24-OCT-1997; 97US-0063121P.

XX PR 24-OCT-1997; 97US-0063127P.

XX PR 24-OCT-1997; 97US-0063128P.

XX PR 27-OCT-1997; 97US-0063327P.

XX PR 27-OCT-1997; 97US-0063329P.

XX PR 28-OCT-1997; 97US-0063341P.

XX PR 28-OCT-1997; 97US-0063342P.

XX PR 28-OCT-1997; 97US-0063344P.

XX PR 28-OCT-1997; 97US-0063349P.

XX PR 28-OCT-1997; 97US-0063550P.

XX PR 28-OCT-1997; 97US-0063564P.

XX PR 28-OCT-1997; 97US-0063435P.

XX PR 28-OCT-1997; 97US-0063704P.

XX PR 28-OCT-1997; 97US-0063732P.

XX PR 28-OCT-1997; 97US-0063734P.

XX PR 28-OCT-1997; 97US-0063735P.

XX PR 28-OCT-1997; 97US-0063738P.

XX PR 29-OCT-1997; 97US-0064115P.

XX PR 31-OCT-1997; 97US-0063870P.

XX PR 31-OCT-1997; 97US-0064103P.

XX PR 03-NOV-1997; 97US-0064248P.

XX PR 12-NOV-1997; 97US-0064809P.

XX PR 17-NOV-1997; 97US-0065186P.

XX PR 18-NOV-1997; 97US-0065846P.

XX PR 21-NOV-1997; 97US-0066120P.

XX PR 21-NOV-1997; 97US-0066364P.

XX PR 24-NOV-1997; 97US-0066453P.

XX PR 24-NOV-1997; 97US-0066466P.

XX PR 24-NOV-1997; 97US-0066511P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 24-NOV-1997; 97US-0066772P.

XX PR 10-SEP-1998; 98WO-US018824.

XX PR 14-SEP-1998; 98WO-US019177.

XX PR 16-SEP-1998; 98WO-US019330.

XX PR 17-SEP-1998; 98WO-US019437.

XX PR 01-DEC-1998; 98WO-US025108.

XX PR 08-SEP-1999; 98WO-US020594.

XX PR 13-SEP-1999; 99WO-US020944.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 15-SEP-1999; 99WO-US021547.

XX PR 05-OCT-1999; 99WO-US023089.

XX PR 29-NOV-1999; 99WO-US028214.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US007177.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.

XX (GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tamas D;
 PI Williams PM, Wood WI;

DR WPI; 2003-147434/14.

DR P-PSDB; ABU54350.

XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
 PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
 PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
 PT disease.

XX Claim 2; Fig 8; 473pp; English.

XX The invention relates to an isolated PRO polypeptide having at least 80%
 CC amino acid sequence identity to: (a) any one of 61 fully defined amino
 CC acid sequences given in the specification (appearing as ABU54347-
 CC ABU54407); (b) an amino acid sequence encoded by the nucleotide sequence
 CC deposited under American Type Culture Collection (accession numbers
 CC listed in the specification); (c) any one of the PRO sequences which
 CC lacks its associated signal peptide; (d) an extracellular domain of the
 CC PRO polypeptide with its associated signal peptide; or (e) an
 CC extracellular domain of the PRO polypeptide which lacks its associated
 CC signal peptide. Also include are the nucleic acids encoding the PRO
 CC polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
 CC polypeptides and nucleic acids are useful in diagnosing or treating
 CC enterocolitis, gastrointestinal ulceration, skin diseases associated with
 CC abnormal keratinocyte differentiation, e.g. psoriasis or epithelial
 CC cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's
 CC disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.
 CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature
 CC aging, AIDS, cancer, diabetic complications, or mutations in general. The
 CC polypeptides are also useful for wound repair and associated therapies
 CC concerned with re-growth of tissue. The nucleotide sequences may be used
 CC as hybridisation probes in chromosome and gene mapping, or in generating
 CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
 CC polypeptides, in assays to identify other proteins or molecules involved
 CC in binding reaction, to generate transgenic animals or knockout animals,
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, for chromosome identification, and
 CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies may be used in
 CC diagnostic assays for PRO, or for the affinity purification of PRO from
 CC recombinant cell culture or natural sources. The present sequence encodes
 CC a PRO polypeptide

SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;

Query Match

100.0%; Score 265; DB 7; Length 960;

Mon Sep 20 09:12:10 2004

us-09-079-874-5.rng

Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCGAGTGGAGAACTGACCCAGCTGGGGAGAGTCTGGACGGCGG 60
DB 85 CGAGGACTGCTGCGAGTGGAGAACTGACCCAGCTGGGGAGAGTCTGGACGGCGG 144
QY 61 CATCCGCGAGTTGCTCTGACCGTCTATCAGCAAGCTGCAGCTTGAACCTGCTGGA 120
DB 145 CATCCGCGAGTTGCTCTGACCGTCTATCAGCAAGCTGCAGCTTGAACCTGCTGGA 204
QY 121 TGACTCACAGGACTACTACGTGGGGAAGAAACATACGTGCTGTGACACGACTTGTG 180
DB 205 TGACTCACAGGACTACTACGTGGGGAAGAAACATACGTGCTGTGACACGACTTGTG 264
QY 181 CAACGCGAGGGGGCCATGCGCTGCGCGCTGCGCGCTGCGCTGCTGCTGCTGCTG 240
DB 265 CAACGCGAGGGGGCCATGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTGCTGCTG 324
QY 241 ACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
DB 325 ACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349

RESULT 13
ACH06793
ID ACH06793 standard; cDNA; 960 BP.
AC ACH06793;
XX XX
DT 08-OCT-2003 (first entry)
XX XX
DE Human secreted/transmembrane polypeptide PRO232 cDNA.
XX XX
KW Human; gene; abnormal bleeding; gynaecological disease; asthma;
KW hystrectomy; angiodysplasia; coronary ischaemic condition; skin disease;
KW gastrointestinal mucosa disorder; acute mucosal lesion; neuropathy; ALS;
KW chronic mucosal lesion; abnormal keratinocyte differentiation; psoriasis;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW uncontrolled cell growth; cancer; blood coagulation cascade; thrombosis;
KW haemorrhage; endometrial bleeding; angiogenesis; wound healing; tumour;
KW tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
XX XX
OS Homo sapiens.
XX XX
PN US2003044839-A1.
XX XX
PD 06-MAR-2003.
XX XX
PF 10-JUL-2001; 2001US-00902903.
XX XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 21-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063707P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98US-0100330P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0101943P.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98US-0109304P.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99US-0146222P.
PR 13-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 05-OCT-1999; 99US-0146222P.
PR 29-NOV-1999; 99US-0146222P.
PR 01-DEC-1999; 99US-0146222P.
PR 02-DEC-1999; 99US-0146222P.
PR 16-DEC-1999; 99US-0146222P.
PR 20-DEC-1999; 99US-0146222P.
PR 05-JAN-2000; 2000US-0000219.
PR 11-FEB-2000; 2000US-0000219.
PR 22-FEB-2000; 2000US-0000219.
PR 24-FEB-2000; 2000US-0000219.
PR 02-MAR-2000; 2000US-0000219.
PR 30-MAR-2000; 2000US-0000219.
PR 22-MAY-2000; 2000US-0000219.
PR 02-JUN-2000; 2000US-0000219.
PR 28-JUL-2000; 2000US-0000219.
PR 24-AUG-2000; 2000US-0000219.
PR 18-SEP-2000; 2000US-0000219.
XX XX
PA (GETH) GENENTECH INC.
XX XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WT;
DR WPI; 2003-492258/46.
DR P-PSDB; ABO47365.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating abnormal bleeding involved in
PT gynecological diseases, skin diseases and neurodegenerative diseases.
XX
XX Claim 3; Fig 8; 478pp; English.
XX
XX The invention relates to an isolated PRO polypeptide. PRO317 is useful in
CC diagnosing or treating abnormal bleeding involved in gynecological
CC diseases e.g. to avoid or lessen the need for hysterectomy. PRO317 may
CC also be useful as an agent that affects angiogenesis and PRO317 is useful
CC in anti-tumour indications or in treating coronary ischaemic conditions.
CC PRO211 and PRO217 polypeptides are useful for treating disorders
CC associated with the preservation and maintenance of gastrointestinal
CC mucosa and the repair of acute and chronic mucosal lesions, skin diseases
CC associated with abnormal keratinocyte differentiation (e.g. psoriasis).
CC PRO197 polypeptide is useful for treating Parkinson's disease,
CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies
CC and disease related to uncontrolled cell growth, e.g. cancer. PRO219
CC polypeptide plays a regulatory role in the blood coagulation cascade.
CC PRO246 polypeptides which serves as tumour specific antigens may be
CC exploited as therapeutic targets for anti-tumour drugs. PRO269
CC polypeptide is useful as an antithrombotic agent with reduced risk for
CC haemorrhage as compared with heparin. PRO317 polypeptide is useful in
CC treating endometrial bleeding angiogenesis. PRO287 polypeptides and
CC portion have therapeutic applications in wound healing and tissue repair.
CC PRO234 polypeptides are useful for treating asthma, rheumatoid arthritis,
CC psoriasis and multiple sclerosis. The polypeptide and its nucleic acid
CC are useful for tissue typing. PRO antibodies are useful for
CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
CC expression in specific cells, tissues or serum and for affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC present sequence represents cDNA encoding a human secreted/transmembrane
CC PRO polypeptide
XX
XX Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;
Query Match 100.0%; Score 265; DB 7; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 60
Db 85 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 144
QY 61 CATCCGCGAGTTGGGCTCTGACCTCATCAGCAAGGCTGCAGCTTGAATGGTGA 120
Db 145 CATCCGCGAGTTGGGCTCTGACCTCATCAGCAAGGCTGCAGCTTGAATGGTGA 204
QY 121 TGACTCAGAGACTACTAGCTGGGCAAGAACATCATCGTGTGACACCGACTTGTG 180
Db 205 TGACTCAGAGACTACTAGCTGGGCAAGAACATCATCGTGTGACACCGACTTGTG 264
QY 181 CAACGCCAGCGGGGCCCATGCCCTGACGGGTGCGGCATCTTTGGCTGCTCCTGC 240
Db 265 CAACGCCAGCGGGGCCCATGCCCTGACGGGTGCGGCATCTTTGGCTGCTCCTGC 324
QY 241 ACTGGGCTCTGCTCTGGGGACC 265
Db 325 ACTGGGCTCTGCTCTGGGGACC 349
RESULT 14
ABX96030
ID ABX96030 standard; cDNA; 960 BP.

XX ABX96030;
XX
XX 13-MAY-2003 (first entry)
XX
XX Human secreted/transmembrane protein cDNA, #5.
XX
XX Human; Gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW diagnostic; biosensor; reactor; therapeutic; hyperplasia;
KW endometriosis; cancer; tumour; ischaemia; coronary arterial disease;
KW polycystic kidney disease; renal failure; inflammatory response; asthma;
KW rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;
KW cytosolic; gynecological; cardiant; nephrotropic; hepatotropic;
KW antiinflammatory.
XX
XX Homo sapiens.
XX
XX US2002160374-A1.
XX
XX 31-OCT-2002.
XX
XX 12-JUL-2001; 2001US-00905291.
XX
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 21-OCT-1997; 97US-0062287P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 29-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 31-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 03-NOV-1997; 97US-0064103P.
XX 07-NOV-1997; 97US-0064248P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066770P.
XX 24-NOV-1997; 97US-0066772P.
XX 10-SEP-1998; 98WO-US018824.

PT or PRO1868, useful in chromosome and gene mapping, in generating
PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease.
XX
PS Example 4; Fig 8; 48pp; English.
XX
CC The invention relates to sixty one nucleic acids encoding PRO
CC polypeptides (secreted and transmembrane). The polynucleotide is useful
CC in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC gene therapy. The polynucleotide may also be used in preparing PRO
CC polypeptides by recombinant techniques, and in generating either
CC transgenic animals or knock-out animals which, in turn, are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptide or the antibody is used in preparing a medicament for
CC treating a condition responsive to the polypeptide or antibody, such as
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
CC atrophica areata, angiogenesis, inflammatory disease e.g. asthma and
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
CC present sequence represents an cDNA which encodes a PRO polypeptide
XX
SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;
Query Match 100.0%; Score 265; DB 7; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGCG 60
DB 85 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGCG 144
QY 61 CATCCGGCAGTGGCTCTCTACCGTATCAGCAAGAGGCTGAGCTTGAACGCGTGA 120
DB 145 CATCCGGCAGTGGCTCTCTACCGTATCAGCAAGAGGCTGAGCTTGAACGCGTGA 204
QY 121 TGACTCAGGACTACTACGTGGGCAAGAGAAATCAGCTGTGTGACACCGACTTTGTG 180
DB 205 TGACTCAGGACTACTACGTGGGCAAGAGAAATCAGCTGTGTGACACCGACTTTGTG 264
QY 181 CAACGCCAGCGGGGCCATGCTGAGCGCGGTGCGCGCATCTCTGGCGTCTCCCTGC 240
DB 265 CAACGCCAGCGGGGCCATGCTGAGCGCGGTGCGCGCATCTCTGGCGTCTCCCTGC 324
QY 241 ACTGGGCTGCTGCTTGGGGACCC 265
DB 325 ACTGGGCTGCTGCTTGGGGACCC 349

Search completed: September 18, 2004, 07:06:59
Job time : 175.233 secs

29-OCT-1997; 97US-0063734P.
29-OCT-1997; 97US-0063738P.
29-OCT-1997; 97US-0063738P.
29-OCT-1997; 97US-0064215P.
31-OCT-1997; 97US-0063870P.
31-OCT-1997; 97US-0064103P.
31-OCT-1997; 97US-0064248P.
07-NOV-1997; 97US-0064803P.
12-NOV-1997; 97US-0065186P.
17-NOV-1997; 97US-0065846P.
18-NOV-1997; 97US-0065693P.
21-NOV-1997; 97US-0066120P.
21-NOV-1997; 97US-0066364P.
24-NOV-1997; 97US-0066453P.
24-NOV-1997; 97US-0066468P.
24-NOV-1997; 97US-0066511P.
24-NOV-1997; 97US-0066770P.
25-NOV-1997; 97US-0066772P.
25-NOV-1997; 97US-0066840P.
12-DEC-1997; 97US-0069425P.
04-JUN-1998; 98US-0088026P.
10-SEP-1998; 98US-0098803P.
14-SEP-1998; 98WO-US018824.
14-SEP-1998; 98US-0100262P.
16-SEP-1998; 98WO-US019177.
17-SEP-1998; 98WO-US019330.
17-SEP-1998; 98US-0100858P.
17-SEP-1998; 98WO-US019437.
13-OCT-1998; 98US-0104080P.
20-NOV-1998; 98US-0109304P.
01-DEC-1998; 98WO-US025108.
22-DEC-1998; 98US-0113296P.
07-JUL-1999; 99US-0114304P.
26-JUL-1999; 99US-0145698P.
28-JUL-1999; 99US-0146222P.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028564.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
03-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US000365.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
XX
FA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-331485/31.
DR P-ESDB; ABU67348.
XX
PT Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245

Blank
Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 06:05:35 ; Search time 30.9574 Seconds
(without alignments)
4750.463 Million cell updates/sec

Title: US-09-079-874-5

Perfect score: 265

Sequence: 1 CGAGGACTGCTGCAGGTGG.....GCTGTGCTCTCGGGAGCC 265

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	265	100.0	960	4	US-09-307-794A-17
2	265	100.0	960	4	US-09-305-125A-17
3	265	100.0	960	4	US-09-302-775A-17
4	265	100.0	938	3	US-09-203-939-1
5	265	100.0	938	3	US-08-251-835-1
6	265	100.0	938	3	US-09-318-503-1
7	265	100.0	938	3	US-09-038-261A-1
8	265	100.0	938	4	US-09-564-329A-1
9	264.6	99.8	494	2	US-08-675-508-4
10	195.8	73.9	286	2	US-08-675-508-21
11	183	69.1	288	3	US-08-675-508-23
12	134.6	50.8	441	3	US-09-203-939-3
13	134.6	50.8	441	3	US-09-251-835-3
14	134.6	50.8	441	3	US-09-318-503-3
15	134.6	50.8	441	3	US-09-038-261A-3
16	134.6	50.8	441	4	US-09-564-329A-3
17	118.4	44.7	232	2	US-08-675-508-25
18	106.2	40.1	251	2	US-08-675-508-22
19	106	40.0	230	2	US-08-675-508-24
20	76	28.7	77	2	US-08-675-508-26
21	39.2	14.8	4060	1	US-08-308-949A-1
22	39	14.7	44	4	US-09-307-794A-21
23	39	14.7	44	4	US-09-305-125A-21
24	39	14.7	44	4	US-09-902-775A-21
25	38.6	14.6	1077	4	US-08-489-039A-2155
26	37.6	14.2	2750	4	US-09-252-991A-6375
27	37.6	14.2	3948	4	US-09-252-991A-6175

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28	37	14.0	933	4	US-09-252-991A-11943	Sequence 11943, A
29	37	14.0	1650	4	US-09-252-991A-11977	Sequence 11977, A
30	36.8	13.9	1125	4	US-09-252-991A-1292	Sequence 1292, Ap
31	36.8	13.9	1152	4	US-09-731-030A-14	Sequence 14, Appl
32	36.8	13.9	1176	4	US-09-731-030A-12	Sequence 12, Appl
33	36.8	13.9	1182	1	US-07-640-476-4	Sequence 4, Appl
34	36.8	13.9	1185	6	5290690-1	Patent No. 5290690
35	36.8	13.9	1554	4	US-09-252-991A-4893	Sequence 4893, Ap
36	36.8	13.9	1566	6	5290690-3	Patent No. 5290690
37	36.8	13.9	1637	3	US-08-852-824-3	Sequence 3, Appl
38	36.8	13.9	1649	2	US-08-845-566-2	Sequence 2, Appl
39	36.8	13.9	1907	4	US-09-399-913-5	Sequence 5, Appl
40	36.8	13.9	1907	4	US-09-298-731-5	Sequence 5, Appl
41	36.8	13.9	2139	4	US-09-252-991A-4910	Sequence 4910, Ap
42	36.8	13.9	2270	4	US-09-731-030A-10	Sequence 10, Appl
43	36.8	13.9	2478	1	US-08-481-626-1	Sequence 1, Appl
44	36.8	13.9	4020	3	US-09-050-159-130	Sequence 130, App
45	36.8	13.9	4020	4	US-09-023-655-1003	Sequence 1003, Ap

ALIGNMENTS

RESULT 1

US-09-307-794A-17
; Sequence 17, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/307,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

us-09-079-874-5.rn.i

Mon Sep 20 09:12:10 2004

/	PRIOR FILING DATE:	1999-09-15
/	PRIOR APPLICATION NUMBER:	PCT/US99/23089
/	PRIOR FILING DATE:	1999-10-05
/	PRIOR APPLICATION NUMBER:	PCT/US99/28214
/	PRIOR FILING DATE:	1999-11-29
/	PRIOR APPLICATION NUMBER:	PCT/US99/28313
/	PRIOR FILING DATE:	1999-11-30
/	PRIOR APPLICATION NUMBER:	PCT/US99/28564
/	PRIOR FILING DATE:	1999-12-02
/	PRIOR APPLICATION NUMBER:	PCT/US99/28565
/	PRIOR FILING DATE:	1999-12-02
/	PRIOR APPLICATION NUMBER:	PCT/US99/30095
/	PRIOR FILING DATE:	1999-12-16
/	PRIOR APPLICATION NUMBER:	PCT/US99/30911
/	PRIOR FILING DATE:	1999-12-20
/	PRIOR APPLICATION NUMBER:	PCT/US99/30999
/	PRIOR FILING DATE:	1999-12-20
/	PRIOR APPLICATION NUMBER:	PCT/US00/00219
/	PRIOR FILING DATE:	2000-01-05
/	NUMBER OF SEQ ID NOS:	423
/	SEQ ID NO 17	
/	LENGTH:	960
/	TYPE:	DNA
/	ORGANISM:	Homo sapiens
/	US-09-907-794A-17	
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Best Local Similarity 100.0%; Pred. No. 4, 6e-57;		
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	CGAGGACTGCCTGCAGGTGGAGAATGTACCCAGTGGGGGAGCAGTGCTGAACCGCGC 60
Db	85	CGAGGACTGCCCTGCAGGTGGAGAATGTACCCAGTGGGGGAGCAGTGCTGAACCGCGC 144
QY	61	CATCGGCGCACTTGGCTCTCTGACCGTCATCACAAAGCGTCCAGCTTGAAC TGGTGGA 120
Db	145	CATCGGCGCACTTGGCTCTCTGACC GTCATCACAAAGCGTCCAGCTTGAAC TGGTGGA 204
QY	121	TGACTCAGGACTACTACTGTGGCAAGAAAGAACATCACGTGCTGTGACACCGATTG TG 180
Db	205	TGACTCAGGACTACTACTGTGGCAAGAAAGAACATCACGTGCTGTGACACCGATTG TG 264
QY	181	CBAACCCAGCGGCCCATCTCCCTGCAGCGCGTGC CGCCATCTTTGGCTGCTCCC TC GC 240
Db	265	CAACGCCAGCGGGGCCCATGCCCTTCAGACCGCTGCGCCATCTTTGGCTGCTCCC TC GC 324
QY	241	ACTCGGCCCTGTGCTCTGGGAGCC 265
b	325	ACTCGGCCCTGTGCTCTGGGAGCC 349

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US-09-905-125A-17
; ORGANISM: Homo sapiens

Query Match      100.0%; Score 265; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 4.6e-57;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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85 CGAGGACTGCTTCAGGTGGAGAAATGACACCGCTGGGGGAGAGAGTGTCTGCACCGCGCG 144
61 CATCCGCGCAGTTGGGCTCTCTACCGCTCATCAGAAAGCTTGCAGCTTGAATCGCTGGGA 120
145 CATCCGCGCAGTTGGGCTCTCTACCGCTCATCAGAAAGCTTGCAGCTTGAATCGCTGGGA 204
121 TGACTCACAGGACTACTAGCTGGGCAAGAGAACATCAGCTGCTGTGTGACACCGACTTGTG 180
205 TGACTCACAGGACTACTAGCTGGGCAAGAGAACATCAGCTGCTGTGTGACACCGACTTGTG 264
181 CACGCCAGCGGGGGCCCATGCCCTGCAGCGCGCTGCCGCCATCCCTTGGCGTGTCCCTTGC 240
265 CACGCCAGCGGGGGCCCATGCCCTGCAGCGCGCTGCCGCCATCCCTTGGCGTGTCCCTTGC 324
Db

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LOCATION: (608)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (615)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (636)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (640)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (646)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (697)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (926)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
US-09-203-939-1

Query Match 100.0%; Score 265; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 4.6e-57;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGCG 60
DB 113 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGCG 172
QY 61 CATCCGCGCAGTTGGCTTCCCTGACGCTCATCAGCAAGGCTGCACTGCGTGA 120
DB 173 CATCCGCGCAGTTGGCTTCCCTGACGCTCATCAGCAAGGCTGCACTGCGTGA 232
QY 121 TGACTCAGAGGACTACTAGTGGGCAAGAATCATCAGTGTGTGACCGGCTGTG 180
DB 233 TGACTCAGAGGACTACTAGTGGGCAAGAATCATCAGTGTGTGACCGGCTGTG 292
QY 181 CAACGCCAGCGGGGCGCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 240
DB 293 CAACGCCAGCGGGGCGCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 352
QY 241 ACTCGGCTGCTGCTTGGGGACCC 265
DB 353 ACTCGGCTGCTGCTTGGGGACCC 377

RESULT 5
US-09-251-835-1
Sequence 1, Application US/09251835A
Patent No. 6261789
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
FILE REFERENCE: 30435.54US12
CURRENT APPLICATION NUMBER: US/09/251,835A
CURRENT FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 998
TYPE: DNA

ORGANISM: HUMAN PSCA (hPSCA)
FEATURE:
NAME/KEY: misc feature
LOCATION: (543)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (580)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (584)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (604)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (608)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (615)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (636)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (640)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (646)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (697)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
NAME/KEY: misc feature
LOCATION: (926)
OTHER INFORMATION: any nucleotide (i.e. a, c, g or t)
US-09-251-835-1

Query Match 100.0%; Score 265; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 4.6e-57;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGCG 60
DB 113 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGACCGCGCG 172
QY 61 CATCCGCGCAGTTGGCTTCCCTGACGCTCATCAGCAAGGCTGCACTGCGTGA 120
DB 173 CATCCGCGCAGTTGGCTTCCCTGACGCTCATCAGCAAGGCTGCACTGCGTGA 232
QY 121 TGACTCAGAGGACTACTAGTGGGCAAGAATCATCAGTGTGTGACCGGCTGTG 180
DB 233 TGACTCAGAGGACTACTAGTGGGCAAGAATCATCAGTGTGTGACCGGCTGTG 292
QY 181 CAACGCCAGCGGGGCGCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 240
DB 293 CAACGCCAGCGGGGCGCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 352
QY 241 ACTCGGCTGCTGCTTGGGGACCC 265
DB 353 ACTCGGCTGCTGCTTGGGGACCC 377

RESULT 6
US-09-318-503-1
Sequence 1, Application US/09318503A
Patent No. 6261791
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US13
CURRENT APPLICATION NUMBER: US/09/318,503A
CURRENT FILING DATE: 1999-05-25

[illegible]

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 IMMEDIATE SOURCE:
 LIBRARY: BLADTUT02
 CLONE: 1312529
 US-08-675-508-23

Query Match 69.1%; Score 183; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 7.7e-37;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTCCCTCAGGTGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 60
 DB 102 CGAGGACTCCCTCAGGTGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 161
 QY 61 CATCCCGCAGTTGGCTCTCCTGACCGTATCAGCAAGGCTCAGCTTGAACCTGGTGA 120
 DB 162 CATCCCGCAGTTGGCTCTCCTGACCGTATCAGCAAGGCTCAGCTTGAACCTGGTGA 221
 QY 121 TGACTCAGGACTACTAGTGGGCAAGAGAACATCAGCTGCTGTGACCGCTTGTG 180
 DB 222 TGACTCAGGACTACTAGTGGGCAAGAGAACATCAGCTGCTGTGACCGCTTGTG 281
 QY 181 CAA 183
 DB 282 CAA 284

RESULT 12

US-09-203-939-3
 ; Sequence 3, Application US/09203939
 ; Patent No. 6258939

GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US11

; CURRENT APPLICATION NUMBER: US/09/203,939

; CURRENT FILING DATE: 2000-12-02

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 09/038,261

; PRIOR FILING DATE: 1998-03-10

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 441

; TYPE: DNA

; ORGANISM: MURINE PSCA (mpSCA)

US-09-203-939-3

Query Match 50.8%; Score 134.6; DB 3; Length 441;

Best Local Similarity 69.7%; Pred. No. 8.2e-25;

Matches 182; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 5 GACTGCTGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATC 64
 DB 100 GACTGCTGAAATGTACAGAACTGCAGCTGGACCACACAGTTGCTTTACATCGGCATC 159
 QY 65 CGCGCAGTTGGCTCTCCTGACCGTATCAGCAAGGCTGACGTTGAACCTGGTGGATGAC 124
 DB 160 CGGGCCATTGGACTCGTGACAGTTATCAGTAAGGCTGCAGTTCACAGTGTGAGGATGAC 219
 QY 125 TCACAGGACTACTACGTTGGGCAAGAGAACATCAGCTGCTGTGACACCGACTTGTGCAAC 184
 DB 220 TCGGAGAACTACTATTGCGCAAGAGAACATCAGTGTGCTACTCTGACCTGTGCAAT 279
 QY 185 GCCAGCGGGGCCCATGCCCTTGCAGCCGGGTGCGGCATCCCTTGGCTGTCCCTGCATC 244

DB 280 GTCAACGGGGCCACACCCCTGAAGCCACCCACCCCTGGGGTGTGTGACCGTGTCTGC 339
 QY 245 GGCTGCTGCTGTGGGGACCC 265
 DB 340 AGCCTGTGCTGTGGGGCTCC 360

RESULT 13

US-09-251-835-3

; Sequence 3, Application US/09251835A

; Patent No. 6261789

GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN

; FILE REFERENCE: 30435.54US12

; CURRENT APPLICATION NUMBER: US/09/251,835A

; CURRENT FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 09/038,261

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 09/203,939

; PRIOR FILING DATE: 1998-12-02

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 441

; TYPE: DNA

; ORGANISM: MURINE PSCA (mpSCA)

US-09-251-835-3

Query Match 50.8%; Score 134.6; DB 3; Length 441;

Best Local Similarity 69.7%; Pred. No. 8.2e-25;

Matches 182; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 5 GACTGCTGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGGCATC 64
 DB 100 GACTGCTGAAATGTACAGAACTGCAGCTGGACCACACAGTTGCTTTACATCGGCATC 159
 QY 65 CGCGCAGTTGGCTCTCCTGACCGTATCAGCAAGGCTGACGTTGAACCTGGTGGATGAC 124
 DB 160 CGGGCCATTGGACTCGTGACAGTTATCAGTAAGGCTGCAGTTCACAGTGTGAGGATGAC 219
 QY 125 TCACAGGACTACTACGTTGGGCAAGAGAACATCAGCTGCTGTGACACCGACTTGTGCAAC 184
 DB 220 TCGGAGAACTACTATTGCGCAAGAGAACATCAGTGTGCTACTCTGACCTGTGCAAT 279
 QY 185 GCCAGCGGGGCCCATGCCCTTGCAGCCGGGTGCGGCATCCCTTGGCTGTCCCTGCATC 244
 DB 280 GTCAACGGGGCCACACCCCTGAAGCCACCCACCCCTGGGGTGTGTGACCGTGTCTGC 339
 QY 245 GGCTGCTGCTGTGGGGACCC 265
 DB 340 AGCCTGTGCTGTGGGGCTCC 360

RESULT 14

US-09-318-503-3

; Sequence 3, Application US/09318503A

; Patent No. 6261791

GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US13

; CURRENT APPLICATION NUMBER: US/09/318,503A

; CURRENT FILING DATE: 1999-05-25

EARLIER APPLICATION NUMBER: 08/814,279
EARLIER FILING DATE: 1997-03-10
EARLIER APPLICATION NUMBER: 60/071,141
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: 60/074,675
EARLIER FILING DATE: 1998-02-13
EARLIER APPLICATION NUMBER: 09/038,261
EARLIER FILING DATE: 1998-03-10
EARLIER APPLICATION NUMBER: 09/203,939
EARLIER FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 09/251,835
EARLIER FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 441
TYPE: DNA
ORGANISM: MURINE PSCA (mpSCA)
US-09-318-503-3

Query Match 50.8%; Score 134.6; DB 3; Length 441;
Best Local Similarity 69.7%; Pred. No. 8.2e-25;
Matches 182; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
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QY 185 GCCAGCGGGGCCCATCGCTGAGCGGGCTGCGCCATCCTTGGGCTGCTCCCTGCACTC 244
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QY 245 GGCTGTCTGCTCTGGGGACCC 265
DB 340 AGCTGTGTGTGGGGCTCC 360

RESULT 15
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Sequence 3, Application US/09038261A
Patent No. 6267960
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
FILE REFERENCE: 30435.54USU1
CURRENT APPLICATION NUMBER: US/09/038,261A
CURRENT FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 441
TYPE: DNA
ORGANISM: MURINE PSCA (mpSCA)
US-09-038-261A-3

Query Match 50.8%; Score 134.6; DB 3; Length 441;
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Matches 182; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 5 GACTGCTCAGGTGGAGAACTGACCCAGCTGGGGAGCAGTGTGGACCGCGGCATC 64
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DB 160 CGGGCCATTGGACTCGTGACAGTTATCAGTAAGGCTGAGCTCACAGTGTGAGGATGAC 219
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QY 185 GCCAGCGGGGCCCATCGCTGAGCGGGCTGCGCCATCCTTGGGCTGCTCCCTGCACTC 244
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 265

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Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 252372180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	265	100.0	960	9	US-09-309-320-17 Sequence 17, Appl
3	265	100.0	960	9	US-09-309-088B-17 Sequence 17, Appl
4	265	100.0	960	9	US-09-309-291A-17 Sequence 17, Appl
5	265	100.0	960	9	US-09-302-853-17 Sequence 17, Appl
6	265	100.0	960	9	US-09-307-824-17 Sequence 17, Appl
7	265	100.0	960	9	US-09-307-841-17 Sequence 17, Appl
8	265	100.0	960	10	US-09-904-011-17 Sequence 17, Appl
9	265	100.0	960	10	US-09-906-742-17 Sequence 17, Appl
10	265	100.0	960	10	US-09-906-813-17 Sequence 17, Appl
11	265	100.0	960	10	US-09-907-613-17 Sequence 17, Appl
12	265	100.0	960	10	US-09-907-942-17 Sequence 17, Appl
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US-09-904-786-17 Sequence 17, Appl
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US-09-302-615-17 Sequence 17, Appl
US-09-903-925-17 Sequence 17, Appl
US-09-906-760A-17 Sequence 17, Appl
US-09-903-823-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-09-080-140-5
; Sequence 5, Application US/09080140
; Publication No. US20040018553A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,140
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/856,653
; FILING DATE: 15-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6105.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-09-080-140-5
;
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo sapiens
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US-09-909-320-17
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Best Local Similarity 100.0%; Pred. No. 2.3e-69;
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; Sequence 17, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
;
QY 1 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG 60
Db 1 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG 60
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QY 61 CATCCGCGAGTGGCTCTGACCGTCAATCAGCAAGGCTCAGCTTGAATGCGTGA 120
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QY 121 TGACTCACAGGACTACTAGTGGGCAAGAGACATCAGTCTGTGACACGACTTGTG 180
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QY 181 CRAAGCCAGCGGGGCCCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTCCCTGC 240
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Query Match 100.0%; Score 265; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 17, Application US/09909088B
; Patent No. US20020145709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-909-088B-17

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Query Match      100.0%; Score 265; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
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      121  TGACTCAGGACTTACTACGTGGGCAAGAGAAATCAGCTGCTGTGACACCCGACTGTG 180
      205  TGACTCAGGACTTACTACGTGGGCAAGAGAAATCAGCTGCTGTGACACCCGACTGTG 264
      181  CAACGCCAGCGGGGCCCATGCTCCCTGCAGCGCGCTGCCGCCATCCTTCGGTGTCTCCCTGC 240
      265  CAACGCCAGCGGGGCCCATGCTCCCTGCAGCGCGCTGCCGCCATCCTTCGGTGTCTCCCTGC 324
      241  ACTCGGCTGCTGCTCTGGGGAACC 265
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; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-909-088B-17

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; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-17

Query Match 100.0%; Score 265; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGTGGGGAGCAGTGTGACCGCGG 60
Db 85 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGTGGGGAGCAGTGTGACCGCGG 144
QY 61 CATCCGGCAGTGGCTCTGACCTCATCAGCAAGGCTCAGCTTGAACCTGGTGA 120
Db 145 CATCCGGCAGTGGCTCTGACCTCATCAGCAAGGCTCAGCTTGAACCTGGTGA 204
QY 121 TGACTCACAGGACTACTACGTGGGCAAGAAACATCAGTCTGTGACACCGATTGTG 180
Db 205 TGACTCACAGGACTACTACGTGGGCAAGAAACATCAGTCTGTGACACCGATTGTG 264
QY 181 CAACGCCAGGGGGCCCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 240
Db 265 CAACGCCAGGGGGCCCATGCCCTGCAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 324
QY 241 ACTCGGCTGCTGCTCTGGGGACCC 265
Db 325 ACTCGGCTGCTGCTCTGGGGACCC 349

RESULT 5
US-09-902-853-17
; Sequence 17, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-902-853-17

Query Match 100.0%; Score 265; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGTGGGGAGCAGTGTGACCGCGG 60
Db 85 CGAGGACTGCTGCAGTGGAGAACTGCACCCAGTGGGGAGCAGTGTGACCGCGG 144
QY 61 CATCCGGCAGTGGCTCTGACCTCATCAGCAAGGCTCAGCTTGAACCTGGTGA 120
Db 145 CATCCGGCAGTGGCTCTGACCTCATCAGCAAGGCTCAGCTTGAACCTGGTGA 204
QY 121 TGACTCACAGGACTACTACGTGGGCAAGAAACATCAGTCTGTGACACCGATTGTG 180
Db 205 TGACTCACAGGACTACTACGTGGGCAAGAAACATCAGTCTGTGACACCGATTGTG 264

; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 17
 ; LENGTH: 960
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-907-841-17

Query Match 100.0%; Score 265; DB 9; Length 960;
 Best Local Similarity 100.0%; Pred. No. 2.8e-69;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGGAGTCTGAGACCGCGC 60
 DB 85 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGGAGTCTGAGACCGCGC 144
 QY 61 CATCCGCGAGTTGGCTCTCCTGACCGTATCAGCAAAAGCTGACGTTGAACGTTGGA 120
 DB 145 CATCCGCGAGTTGGCTCTCCTGACCGTATCAGCAAAAGCTGACGTTGAACGTTGGA 204
 QY 121 TGACTCACAGGACTACTAGTGGGGAAGAAATCATCGTGTGTGACCCGACTTGTG 180
 DB 205 TGACTCACAGGACTACTAGTGGGGAAGAAATCATCGTGTGTGACCCGACTTGTG 264
 QY 181 CAACGCCAGCGGGCCCATGCCCTGCAGCGCTGCCCGCTCTTGGCTGCTCCCTGC 240
 DB 265 CAACGCCAGCGGGCCCATGCCCTGCAGCGCTGCCCGCTCTTGGCTGCTCCCTGC 324
 QY 241 ACTCGGCTGTGCTCTTGGGACCC 265
 DB 325 ACTCGGCTGTGCTCTTGGGACCC 349

RESULT 8

US-09-904-011-17
 ; Sequence 17, Application US/09904011
 ; Publication No. US20030003530A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/904,011
 ; CURRENT FILING DATE: 2001-07-11
 ; PRIOR APPLICATION NUMBER: 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 17
 ; LENGTH: 960
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-904-011-17

Query Match 100.0%; Score 265; DB 10; Length 960;
 Best Local Similarity 100.0%; Pred. No. 2.8e-69;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGGAGTCTGAGACCGCGC 60
 DB 85 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGGAGTCTGAGACCGCGC 144
 QY 61 CATCCGCGAGTTGGCTCTCCTGACCGTATCAGCAAAAGCTGACGTTGAACGTTGGA 120
 DB 145 CATCCGCGAGTTGGCTCTCCTGACCGTATCAGCAAAAGCTGACGTTGAACGTTGGA 204
 QY 121 TGACTCACAGGACTACTAGTGGGGAAGAAATCATCGTGTGTGACCCGACTTGTG 180

Db 205 TGACTCACAGGACTACTACGTGGCAAGAAGAACATCATCGTCTGTGTGACACCGACTTTGTG 264
QY 181 CAAGCCACGGGGCCCTGCTGAGCCGGCTCCCGCATCTCTTGGCTGTGCTCCCTGC 240
Db 265 CAAGCCACGGGGCCCTGCTGAGCCGGCTCCCGCATCTCTTGGCTGTGCTCCCTGC 324
QY 241 ACTCGGCTGTGCTCTGGGGACCC 265
Db 325 ACTCGGCTGTGCTCTGGGGACCC 349

RESULT 9

US-09-906-742-17
; Sequence 17, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-17
Query Match 100.0%; Score 265; DB 10; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGAGTGTGACCCGCGC 60
Db 85 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGGAGAGTGTGACCCGCGC 144
QY 61 CATCCGCGCAGTTGGCCTCTCTGACCCGTATCAGCAAAAGGCTGCAGCTTGAATCGGTGA 120
Db 145 CATCCGCGCAGTTGGCCTCTCTGACCCGTATCAGCAAAAGGCTGCAGCTTGAATCGGTGA 204
QY 121 TGACTCACAGGACTACTACGTGGGCAAGAAAGATCATCAGCTGTGTGACACCGACTTGTG 180
Db 205 TGACTCACAGGACTACTACGTGGGCAAGAAAGATCATCAGCTGTGTGACACCGACTTGTG 264
QY 181 CAAGCCACGGGGCCCTGCTGAGCCGGCTCCCGCATCTCTTGGCTGTGCTCCCTGC 240
Db 265 CAAGCCACGGGGCCCTGCTGAGCCGGCTCCCGCATCTCTTGGCTGTGCTCCCTGC 324
QY 241 ACTCGGCTGTGCTCTGGGGACCC 265
Db 325 ACTCGGCTGTGCTCTGGGGACCC 349

RESULT 10

US-09-906-838-17
; Sequence 17, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 17
LENGTH: 960
TYPE: DNA
ORGANISM: Homo Sapien
US-09-906-838-17

Query Match 100.0%; Score 265; DB 10; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGAGGACTCCCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG	60
Db	85	CGAGGACTCCCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG	144
QY	61	CATCCCGCAGTTGGCTCTCCTCAGCGTATCAGCAAGAGCTGCAGCTTGAACCTGGTGA	120
Db	145	CATCCCGCAGTTGGCTCTCCTCAGCGTATCAGCAAGAGCTGCAGCTTGAACCTGGTGA	204
QY	121	TGACTCACAGGACTACTAGCTGGGAGAGACATCAGTGTGTGACACCGACTTGTG	180
Db	205	TGACTCACAGGACTACTAGCTGGGAGAGACATCAGTGTGTGACACCGACTTGTG	264
QY	181	CAACGCCAGCGGGGCCATCCCTCAGCGGCTGCAGCGGCTGCAGCGGCTGCAGCGGCTGC	240
Db	265	CAACGCCAGCGGGGCCATCCCTCAGCGGCTGCAGCGGCTGCAGCGGCTGCAGCGGCTGC	324
QY	241	ACTCGGCTGTCTCTCTGGGACCC	265
Db	325	ACTCGGCTGTCTCTCTGGGACCC	349

RESULT 11

US-09-907-613-17

Sequence 17, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Pan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 17
LENGTH: 960
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-613-17

Query Match 100.0%; Score 265; DB 10; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTGCGAGTGGAGAACTGACCCAGCTGGGGAGAGAGTCTGGACCGCGG 60
DB 85 CGAGGACTGCTGCGAGTGGAGAACTGACCCAGCTGGGGAGAGAGTCTGGACCGCGG 144

QY 61 CATCCGCGAGTTGGCTCTGACCGTTCATCAGCAAAGGCTGCAGCTTGAACCTGGTGA 120
DB 145 CATCCGCGAGTTGGCTCTGACCGTTCATCAGCAAAGGCTGCAGCTTGAACCTGGTGA 204

QY 121 TGACTCAGAGTACTACTAGTGGGCAAGAAATCATCGTCTGTGACACCGACTTGTG 180
DB 205 TGACTCAGAGTACTACTAGTGGGCAAGAAATCATCGTCTGTGACACCGACTTGTG 264

QY 181 CAAAGCCAGCGGGGCGGCTGCGCTGACCGGCTGCGGCTGCTGCTGCTGCTGCTGCTG 240
DB 265 CAAAGCCAGCGGGGCGGCTGCGCTGACCGGCTGCGGCTGCTGCTGCTGCTGCTGCTG 324

QY 241 ACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
DB 325 ACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349

RESULT 12
US-09-907-942-17
; Sequence 17, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10468-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13

QY 1 CGAGGACTGCTGCGAGTGGAGAACTGACCCAGCTGGGGAGAGAGTCTGGACCGCGG 60
DB 85 CGAGGACTGCTGCGAGTGGAGAACTGACCCAGCTGGGGAGAGAGTCTGGACCGCGG 144

QY 61 CATCCGCGAGTTGGCTCTGACCGTTCATCAGCAAAGGCTGCAGCTTGAACCTGGTGA 120
DB 145 CATCCGCGAGTTGGCTCTGACCGTTCATCAGCAAAGGCTGCAGCTTGAACCTGGTGA 204

QY 121 TGACTCAGAGTACTACTAGTGGGCAAGAAATCATCGTCTGTGACACCGACTTGTG 180
DB 205 TGACTCAGAGTACTACTAGTGGGCAAGAAATCATCGTCTGTGACACCGACTTGTG 264

QY 181 CAAAGCCAGCGGGGCGGCTGCGCTGACCGGCTGCGGCTGCTGCTGCTGCTGCTGCTG 240
DB 265 CAAAGCCAGCGGGGCGGCTGCGCTGACCGGCTGCGGCTGCTGCTGCTGCTGCTGCTG 324

QY 241 ACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
DB 325 ACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349

RESULT 13
US-09-904-859-17
; Sequence 17, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 17
LENGTH: 960
TYPE: DNA
ORGANISM: Homo Sapien
US-09-904-859-17

Query Match 100.0%; Score 265; DB 10; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGGAGCAGTGTCTGGACCGGCG 60
DB 85 CGAGGACTGCTGCAGGTGGAGAACTGACCCAGCTGGGGGAGCAGTGTCTGGACCGGCG 144
QY 61 CATCCGCGAGTTGGCTCTCCTACCGTATCAGCAAGGCTGCAGCTTGAACTCGGTGGA 120
DB 145 CATCCGCGAGTTGGCTCTCCTACCGTATCAGCAAGGCTGCAGCTTGAACTCGGTGGA 204
QY 121 TGACTCAGAGGACTACTAGTGGGCAAGAAACATACAGTGTGTGACACCGACTTGTG 180

DB 205 TGACTCAGAGGACTACTAGTGGGCAAGAAACATACAGTGTGTGACACCGACTTGTG 264
QY 181 CAAGCGCAGCGGGCCCATGCTCCCTGCAGCGCGGTGCGGCATCTTGTGCGTGTCTCCCTGC 240
DB 265 CAAGCGCAGCGGGCCCATGCTCCCTGCAGCGCGGTGCGGCATCTTGTGCGTGTCTCCCTGC 324
QY 241 ACTCGGCTGTCTGTCTGTGGGACCC 265
DB 325 ACTCGGCTGTCTGTCTGTGGGACCC 349

RESULT 14
US-09-909-204-17
Sequence 17, Application US/09909204
Publication No. US20030036061A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10456-14
CURRENT APPLICATION NUMBER: US/09/909,204
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095

;
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-204-17

Query Match 100.0%; Score 265; DB 10; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 60
Db 85 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 144

Qy 61 CATCGGGCAGTTGGCTCTCTGACCGTCAATCAGCAAGGCTGCAGCTTGAATGGTGA 120
Db 145 CATCGGGCAGTTGGCTCTCTGACCGTCAATCAGCAAGGCTGCAGCTTGAATGGTGA 204

Qy 121 TGACTCAGGACTACTACGTGGGCAAGAAACATCAGCTGTGTGACACCGACTTGTG 180
Db 205 TGACTCAGGACTACTACGTGGGCAAGAAACATCAGCTGTGTGACACCGACTTGTG 264

Qy 181 CAACGCCAGCGGGCCCATGCGCTGTGACCGGCTGGCGCATCTTGGCGTGTCCCTGC 240
Db 265 CAACGCCAGCGGGCCCATGCGCTGTGACCGGCTGGCGCATCTTGGCGTGTCCCTGC 324

Qy 241 ACTCGGCTGTGTCTGTGGGACCC 265
Db 325 ACTCGGCTGTGTCTGTGGGACCC 349

RESULT 15

US-09-904-820-17
; Sequence 17, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Christopher J.
; APPLICANT: Grimaldi, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820

;
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-820-17

Query Match 100.0%; Score 265; DB 10; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 60
Db 85 CGAGGACTGCTGCAGGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 144

Qy 61 CATCGGGCAGTTGGCTCTCTGACCGTCAATCAGCAAGGCTGCAGCTTGAATGGTGA 120
Db 145 CATCGGGCAGTTGGCTCTCTGACCGTCAATCAGCAAGGCTGCAGCTTGAATGGTGA 204

Qy 121 TGACTCAGGACTACTACGTGGGCAAGAAACATCAGCTGTGTGACACCGACTTGTG 180
Db 205 TGACTCAGGACTACTACGTGGGCAAGAAACATCAGCTGTGTGACACCGACTTGTG 264

Qy 181 CAACGCCAGCGGGCCCATGCGCTGTGACCGGCTGGCGCATCTTGGCGTGTCCCTGC 240
Db 265 CAACGCCAGCGGGCCCATGCGCTGTGACCGGCTGGCGCATCTTGGCGTGTCCCTGC 324

Qy 241 ACTCGGCTGTGTCTGTGGGACCC 265
Db 325 ACTCGGCTGTGTCTGTGGGACCC 349

Search completed: September 18, 2004, 20:20:22
Job time : 199.605 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 05:54:35 ; Search time 1211.82 Seconds
(without alignments)
6530.246 Million cell updates/sec

Title: US-09-079-874-5

Perfect score: 265
Sequence: 1 CGAGGACTGCTGCAGGTGG.....GCTCTGCTCTGGGACCC 265

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estmuv:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_man:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	265	100.0	424	12	BM768967 K-EST0052
3	265	100.0	470	13	BQ083505 K-EST0146
4	265	100.0	480	12	BM819937 K-EST0088

5	265	100.0	527	13	BQ083498 K-EST0146
6	265	100.0	550	14	CB147558 K-EST0203
7	265	100.0	682	12	BM042219 603616172
8	265	100.0	692	12	EG761095 602717425
9	265	100.0	735	12	BM041997 603615880
10	265	100.0	748	12	EG765417 602738887
11	265	100.0	827	12	BM018750 603646652
12	265	100.0	880	13	BU157227 AGENCOURT
13	265	100.0	911	13	BU194301 AGENCOURT
14	265	100.0	922	13	BU168360 AGENCOURT
15	265	100.0	924	13	BU174317 AGENCOURT
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17	265	100.0	1024	8	BC023582 Homo sapi
18	265	100.0	1096	13	BU838702 AGENCOURT
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20	263.4	99.4	547	12	BM828076 K-EST0100
21	263.4	99.4	749	12	BM042052 603616054
22	263.4	99.4	820	14	CB956183 AGENCOURT
23	263.4	99.4	901	13	BU173702 AGENCOURT
24	263.4	99.4	924	13	BQ678675 AGENCOURT
25	263.4	99.4	936	13	BU174241 AGENCOURT
26	263.4	99.4	957	13	BQ876328 AGENCOURT
27	263.4	99.4	970	13	BU179764 AGENCOURT
28	263.4	99.4	978	13	BQ680817 AGENCOURT
29	263.4	99.4	990	11	EC048808 Homo sapi
30	263.4	99.4	1009	13	BU168445 AGENCOURT
31	261.8	98.8	843	14	CB997275 AGENCOURT
32	261.8	98.8	851	14	CB993163 AGENCOURT
33	252.4	95.2	571	12	BI763453 603047463
34	242	91.3	642	12	BI253841 602974614
35	201.8	76.2	315	12	BM750435 K-EST0026
36	198.4	74.9	671	12	BM817901 K-EST0084
37	144.4	54.5	237	9	AA476643 zw85f03.r
38	135.2	51.0	401	13	BY093000 BY093000
39	134.6	50.8	320	29	AY418124 Mus muscu
40	134.6	50.8	386	13	BY088484 BY088484
41	134.6	50.8	388	13	BY088363 BY088363
42	134.6	50.8	414	14	W11983 ma80f09.r1
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44	134.6	50.8	431	9	AA107101 ml93b04.r
45	134.6	50.8	447	14	W42223 mb16b10.r1

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Pan troglodytes HCM6452 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY418123
VERSION AY418123.1 GI:39774083
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 316)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 316)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
source
1. 316
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
c1_>316
/locus_tag="HCM6452"

gene

ORIGIN

Query Match 100.0%; Score 265; DB 29; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.4e-45;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCCGGG 60
Db 44 CGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCCGGG 103
QY 61 CATCCGGCGAGTTGGCCCTCTGACCTGATCAGCAAGGCTGCGAGCTTGAAGTGGTGA 120
Db 104 CATCCGGCGAGTTGGCCCTCTGACCTGATCAGCAAGGCTGCGAGCTTGAAGTGGTGA 163
QY 121 TGACTCAGAGACTACTACGTGGGCAAGAGACATCAGTGTGTGACACCGACTTTGT 180
Db 164 TGACTCAGAGACTACTACGTGGGCAAGAGACATCAGTGTGTGACACCGACTTTGT 223
QY 181 CAAGCCAGCGGGGCCCATCCCTGTCAGCGGGTGGCGGCATCTTGGCCTGCTCCCTGC 240
Db 224 CAAGCCAGCGGGGCCCATCCCTGTCAGCGGGTGGCGGCATCTTGGCCTGCTCCCTGC 283
QY 241 ACTCGGCTGCTGCTTGGGGACCC 265
Db 284 ACTCGGCTGCTGCTTGGGGACCC 308

RESULT 2
LOCUS BM768967
DEFINITION K-EST0052116 S14K402 Homo sapiens cDNA clone S14K402-13-D04 5', mRNA sequence.

ACCESSION BM768967.1 GI:19098582
VERSION BM768967.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 424)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 13 row: D column: 04
High quality sequence stop: 424.
Location/Qualifiers
1. 424
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-13-D04"
/cell_line="K402"
/lab_host="Top10F"

FEATURES
source
1. 424
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-13-D04"
/cell_line="K402"
/lab_host="Top10F"

clone lib="S14K402"
/note="Organ: Stomach; Vector: pTZ189Pl; Site: 1: EcoRI; Site: 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dn-selected mRNA by priming with dn-tailed vector. The dn-tailed vector was adjusted to have about 60nt. The cDNA vector was then circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 265; DB 12; Length 424;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCCGGG 60
Db 153 CGAGGACTGCTGCGAGTGGAGAACTGCACCCAGCTGGGGGAGCAGTCTGACCCGGG 212
QY 61 CATCCGGCGAGTTGGCCCTCTGACCTGATCAGCAAGGCTGCGAGCTTGAAGTGGTGA 120
Db 213 CATCCGGCGAGTTGGCCCTCTGACCTGATCAGCAAGGCTGCGAGCTTGAAGTGGTGA 272
QY 121 TGACTCAGAGACTACTACGTGGGCAAGAGACATCAGTGTGTGACACCGACTTTGT 180
Db 273 TGACTCAGAGACTACTACGTGGGCAAGAGACATCAGTGTGTGACACCGACTTTGT 332
QY 181 CAAGCCAGCGGGGCCCATCCCTGTCAGCGGGTGGCGGCATCTTGGCCTGCTCCCTGC 240
Db 333 CAAGCCAGCGGGGCCCATCCCTGTCAGCGGGTGGCGGCATCTTGGCCTGCTCCCTGC 392
QY 241 ACTCGGCTGCTGCTTGGGGACCC 265
Db 393 ACTCGGCTGCTGCTTGGGGACCC 417

RESULT 3
LOCUS BQ083505
DEFINITION K-EST0146186 S14K402 Homo sapiens cDNA clone S14K402-65-D08 5', mRNA sequence.

ACCESSION BQ083505
VERSION BQ083505.1 GI:19942340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 65 row: D column: 08
High quality sequence stop: 470.
Location/Qualifiers
1. 470

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-65-D08"
/cell_line="K402"
/lab_host="Top10F"
/clone_lib="S14K402"
/notes="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 100.0%; Score 265; DB 13; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGAGCTGCTCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG 60
Db 153 CGAGGAGTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG 212
QY 61 CATCCGCGAGTTGGCTCTGACCTCATTCAGCAAAAGCTGCAGCTTGAATGCGTGA 120
Db 213 CATCCGCGAGTTGGCTCTGACCTCATTCAGCAAAAGCTGCAGCTTGAATGCGTGA 272
QY 121 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTCTGACACCGACTTGG 180
Db 273 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTCTGACACCGACTTGG 332
QY 181 CAACGCCAGCGGGGCCATGCTCCCTGCGCGGCTGCGCCATCTTGCCTGCTCCCTGC 240
Db 333 CAACGCCAGCGGGGCCATGCTCCCTGCGCGGCTGCGCCATCTTGCCTGCTCCCTGC 392
QY 241 ACTCGGCTGCTGCTCTGGGACCC 265
Db 393 ACTCGGCTGCTGCTCTGGGACCC 417

RESULT 4
BM819937 480 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0088167 S18N669761 Homo sapiens cDNA clone S18N669761-19-E04
DEFINITION 5', mRNA sequence.
ACCESSION BM819937
VERSION BM819937.1 GI:19176350
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 480)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470

Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 19 row: E column: 04
High quality sequence stop: 480.
Location/Qualifiers
1..480
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-19-E04"
/sex="F"
/lab_host="Top10F"
/clone_lib="S18N669761"
/notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 100.0%; Score 265; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGAGTGCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG 60
Db 113 CGAGGAGTGCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGG 172
QY 61 CATCCGCGAGTTGGCTCTGACCTCATTCAGCAAAAGCTGCAGCTTGAATGCGTGA 120
Db 173 CATCCGCGAGTTGGCTCTGACCTCATTCAGCAAAAGCTGCAGCTTGAATGCGTGA 232
QY 121 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTCTGACACCGACTTGG 180
Db 233 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTGTCTGACACCGACTTGG 292
QY 181 CAACGCCAGCGGGGCCATGCTCCCTGCGCGGCTGCGCCATCTTGCCTGCTCCCTGC 240
Db 293 CAACGCCAGCGGGGCCATGCTCCCTGCGCGGCTGCGCCATCTTGCCTGCTCCCTGC 352
QY 241 ACTCGGCTGCTGCTCTGGGACCC 265
Db 353 ACTCGGCTGCTGCTCTGGGACCC 377

RESULT 5
BQ083498
LOCUS K-EST0146178 S14K402 Homo sapiens cDNA clone S14K402-65-C11 5',
DEFINITION mRNA sequence.
ACCESSION BQ083498
VERSION BQ083498.1 GI:19942325
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 527)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001

JOURNAL
COMMENT

Unpublished (2002)
Contact: Kim YS
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 65, row: C column: 11
High quality sequence stop: 527.
Location/Qualifiers
1. 527

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-65-C11"
/cell_line="K402"
/lab_host="Top10F"
/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ19RPI; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 265; DB 13; Length 527;

Best Local Similarity 100.0%; Pred. No. 1,1e-44;

Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGACTGCTGAGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTCGACCGCGC 60
Db 153 CGAGACTGCTGAGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTCGACCGCGC 212
QY 61 CATCCGCGCAGTTGGCTCTGACCTGATCAGCAAGGCTGACGTTGAAGTGGTGA 120
Db 213 CATCCGCGCAGTTGGCTCTGACCTGATCAGCAAGGCTGACGTTGAAGTGGTGA 272
QY 121 TGACTCAGGACTACTACGTGGGGAAGAACATCAGCTGCTGTGACACGACTTGTG 180
Db 273 TGACTCAGGACTACTACGTGGGGAAGAACATCAGCTGCTGTGACACGACTTGTG 332
QY 181 CAACGCCAGCGGGGCCCATCCCTCGAGCGGGCTGCGGCCATCTTGGGCTGCTCCCTGC 240
Db 333 CAACGCCAGCGGGGCCCATCCCTCGAGCGGGCTGCGGCCATCTTGGGCTGCTCCCTGC 392
QY 241 ACTCGGCTGCTGCTTGGGGACCC 265
Db 393 ACTCGGCTGCTGCTTGGGGACCC 417

RESULT 6

CB147558 550 bp mRNA linear EST 29-JAN-2003
LOCUS X-EST0203584 L11SN354s1 Homo sapiens cDNA clone L11SN354s1-29-C07
DEFINITION 5', mRNA sequence.
ACCESSION CB147558
VERSION CB147558.1 GI:28129015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 550)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)

TITLE

JOURNAL

COMMENT

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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29, row: C column: 07
High quality sequence stop: 550.
Location/Qualifiers
1. 550

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L11SN354s1-29-C07"
/sex="M"
/tissue_type="Liver"
/cell_type="Polygonal"
/cell_line="SNU-354"
/lab_host="Top10F"
/clone_lib="L11SN354s1"

/note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F with electroporation method."

ORIGIN

Query Match 100.0%; Score 265; DB 14; Length 550;

Best Local Similarity 100.0%; Pred. No. 1,1e-44;

Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGACTGCTGAGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTCGACCGCGC 60
Db 113 CGAGACTGCTGAGTGAGAACTGCACCCAGCTGGGGAGAGAGTGTCGACCGCGC 172
QY 61 CATCCGCGCAGTTGGCTCTGACCTGATCAGCAAGGCTGACGTTGAAGTGGTGA 120
Db 173 CATCCGCGCAGTTGGCTCTGACCTGATCAGCAAGGCTGACGTTGAAGTGGTGA 232
QY 121 TGACTCAGGACTACTACGTGGGGAAGAACATCAGCTGCTGTGACACCGACTTGTG 180

Db 233 TGACTCACAGGACTACTAGTGGGCAAGAGACATCAGTGTGTGACACCGACTTGTG 292

Qy 181 CAACGCCAGGGGGCCCAATGCCCTGACGCCGCTGCGGCATCTTGGCTGCTCCCTGC 240

Db 293 CAACGCCAGGGGGCCCAATGCCCTGACGCCGCTGCGGCATCTTGGCTGCTCCCTGC 352

Qy 241 ACTCGGCTGTGCTGCTGCGGACCC 265

Db 353 ACTCGGCTGTGCTGCTGCGGACCC 377

RESULT 7
 BM042219
 LOCUS 603616172F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5557096 5',
 DEFINITION mRNA sequence.
 ACCESSION BM042219
 VERSION EST.
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 682)
 NIH-MGC http://img.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCID/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM201 row: o column: 17
 High quality sequence stop: 678.

FEATURES
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 1. .682
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5557096"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 265; DB 12; Length 682;
 Best Local Similarity 100.0%; Pred. No. 1.2e-44;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 60
 Db 103 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 162
 Qy 61 CATCCCGCAGTTGGCTCTTCAACCGTATCAGAAAGGCTGCAGCTTGAACCTGGTGA 120
 Db 163 CATCCCGCAGTTGGCTCTTCAACCGTATCAGAAAGGCTGCAGCTTGAACCTGGTGA 222
 Qy 121 TGACTCACAGGACTACTAGTGGGCAAGAGACATCAGTGTGTGACACCGACTTGTG 180
 Db 223 TGACTCACAGGACTACTAGTGGGCAAGAGACATCAGTGTGTGACACCGACTTGTG 282

Qy 181 CAACGCCAGGGGGCCCAATGCCCTGACGCCGCTGCGGCATCTTGGCTGCTCCCTGC 240

Db 283 CAACGCCAGGGGGCCCAATGCCCTGACGCCGCTGCGGCATCTTGGCTGCTCCCTGC 342

Qy 241 ACTCGGCTGTGCTGCTGCGGACCC 265

Db 343 ACTCGGCTGTGCTGCTGCGGACCC 367

RESULT 8
 BG761095
 LOCUS 602717428F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4840974 5',
 DEFINITION mRNA sequence.
 ACCESSION BG761095
 VERSION EST.
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 692)
 NIH-MGC http://img.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1673 row: a column: 07
 High quality sequence stop: 690.

FEATURES
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 1. .692
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4840974"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 49"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN
 Query Match 100.0%; Score 265; DB 12; Length 692;
 Best Local Similarity 100.0%; Pred. No. 1.2e-44;
 Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 60
 Db 103 CGAGGACTCCCTGCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGACCGCGC 162
 Qy 61 CATCCCGCAGTTGGCTCTTCAACCGTATCAGAAAGGCTGCAGCTTGAACCTGGTGA 120
 Db 163 CATCCCGCAGTTGGCTCTTCAACCGTATCAGAAAGGCTGCAGCTTGAACCTGGTGA 222
 Qy 121 TGACTCACAGGACTACTAGTGGGCAAGAGACATCAGTGTGTGACACCGACTTGTG 180
 Db 223 TGACTCACAGGACTACTAGTGGGCAAGAGACATCAGTGTGTGACACCGACTTGTG 282
 Qy 181 CAACGCCAGGGGGCCCAATGCCCTGACGCCGCTGCGGCATCTTGGCTGCTCCCTGC 240

283 CAACGCCAGCGGGCCATGCTGCGAGCGGCTGCCGCCATCCTTGGCTGCTCCCTGC 342

241 ACTCGGCTGCTGCTCTGGGACCC 265

343 ACTCGGCTGCTGCTCTGGGACCC 367

RESULT 9

LOCUS BM041997 735 bp mRNA linear EST 07-NOV-2001

DEFINITION 603615880F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420779 5', mRNA sequence.

ACCESSION BM041997

VERSION BM041997.1 GI:16771264

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 735)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: L16M1875 row: 0 column: 20

High quality sequence stop: 733.

Location/Qualifiers

1..735

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5420779"

/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 112"

/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 265; DB 12; Length 735;

Best Local Similarity 100.0%; Pred. No. 1.2e-44;

Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGACTGCTCGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 60

DB 15 CGAGGACTGCCTGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 74

QY 61 CATCCGGCAGTTGGCTCTGACCGTATCAGCAAGCTGAGCTTGAACCTGCTGA 120

DB 75 CATCCGGCAGTTGGCTCTGACCGTATCAGCAAGCTGAGCTTGAACCTGCTGA 134

QY 121 TGACTCAGAGTACTTACCTGCGGCAAGAACATCAGCTGTGTGACCGACTTTGT 180

DB 135 TGACTCAGAGTACTTACCTGCGGCAAGAACATCAGCTGTGTGACCGACTTTGT 194

QY 181 CAACGCCAGCGGGCCATCCTGTCGAGCGGCTGCCGATCCTTGGCTGCTCCCTGC 240

DB 195 CAACGCCAGCGGGCCATCCTGTCGAGCGGCTGCCGATCCTTGGCTGCTCCCTGC 254

241 ACTCGGCTGCTGCTCTGGGACCC 265

255 ACTCGGCTGCTGCTCTGGGACCC 279

RESULT 10

LOCUS BG765417 748 bp mRNA linear EST 15-MAY-2001

DEFINITION 602738887F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4868924 5', mRNA sequence.

ACCESSION BG765417

VERSION BG765417.1 GI:14076070

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 748)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: L16M1739 row: m column: 21

High quality sequence stop: 743.

Location/Qualifiers

1..748

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4868924"

/tissue_type="melanotic melanoma, high MDR (cell line)"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 49"

/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 285; DB 12; Length 748;

Best Local Similarity 100.0%; Pred. No. 1.2e-44;

Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 97 CGAGGACTGCCTGAGTGGAGAACTGCACCCAGCTGGGGAGCAGTGTGGACCGCGG 156

QY 61 CATCCGGCAGTTGGCTCTGACCGTATCAGCAAGCTGAGCTTGAACCTGCTGA 120

DB 157 CATCCGGCAGTTGGCTCTGACCGTATCAGCAAGCTGAGCTTGAACCTGCTGA 216

QY 121 TGACTCAGAGTACTTACCTGCGGCAAGAACATCAGCTGTGTGACCGACTTTGT 180

DB 217 TGACTCAGAGTACTTACCTGCGGCAAGAACATCAGCTGTGTGACCGACTTTGT 276

QY 181 CAACGCCAGCGGGCCATCCTTGCAGCGGCTGCCGATCCTTGGCTGCTCCCTGC 240

DB 277 CAACGCCAGCGGGCCATCCTTGCAGCGGCTGCCGATCCTTGGCTGCTCCCTGC 336

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QY 241 ACTCGGCTGCTGCTCTGGGACCC 265
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Db 337 ACTCGGCTGCTGCTCTGGGACCC 361

RESULT 11
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DEFINITION mRNA sequence.
ACCESSION BM018750
VERSION BM018750.1 GI:16533104
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 827)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1895 row: 9 column: 14
High quality sequence stop: 810.
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/clone="IMAGE:5428261"
/tissue_type="astrocytoma grade IV, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_98"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 265; DB 12; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CATCCGCGCAGTTGGCTCTTACCGCTCATCAGCAAGGCTGCAGCTTGAACCTGCGTGA 120
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 265; DB 13; Length 880;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 CAACGCCACGGGGCCCATGCCCTGCAGCCGCTGCCGCAATCCCTTGGCTGCTCCCTGC 240
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5', mRNA sequence.
ACCESSION  BUI94301
VERSION    BUI94301.1 GI:22708285
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 911)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DTP
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2347 row: a column: 14
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             /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GGCACGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."
ORIGIN
Query Match 100.0%; Score 265; DB 13; Length 911;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 70 CATCCGCGCAGTTGGCTCTCAGCGTCATCAGCAAGGCTGCAGCTTGAACCTGCTGA 129
QY 121 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTCTGTGACACCGACTTTGTG 180
DB 130 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTCTGTGACACCGACTTTGTG 189
QY 181 CAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGCATCTTTGCGCTGCTCCCTGC 240
DB 190 CAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGCATCTTTGCGCTGCTCCCTGC 249
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BUI68360
LOCUS      BUI68360
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5', mRNA sequence.
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VERSION    BUI68360.1 GI:22682344
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 922)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DTP
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
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           High quality sequence stop: 597.
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             /lab_host="DH10B (phage-resistant)"
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             /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GGCACGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e-44;
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DB 11 CGAGGACTGCTTCAGTGGAGACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCG 70
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RESULT 15
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VERSION    BUI74317.1 GI:22682344
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 922)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DTP
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2359 row: f column: 09
           High quality sequence stop: 597.
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             /clone_lib="NIH MGC 112"
             /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GGCACGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."
ORIGIN
Query Match 100.0%; Score 265; DB 13; Length 922;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAGGACTGCTTCAGTGGAGACTGCACCCAGCTGGGGAGCAGTGTGACCGCGCG 60
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QY 61 CATCCGCGCAGTTGGCTCTCAGCGTCATCAGCAAGGCTGCAGCTTGAACCTGCTGA 120
DB 71 CATCCGCGCAGTTGGCTCTCAGCGTCATCAGCAAGGCTGCAGCTTGAACCTGCTGA 130
QY 121 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTCTGTGACACCGACTTTGTG 180
DB 131 TGACTCACAGGACTACTAGTGGGCAAGAGAACATCAGTCTGTGACACCGACTTTGTG 190
QY 181 CAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGCATCTTTGCGCTGCTCCCTGC 240
DB 191 CAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGCATCTTTGCGCTGCTCCCTGC 250
QY 241 ACTCGGCTGCTGCTCTGGGGACCC 265
DB 251 ACTCGGCTGCTGCTCTGGGGACCC 275

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DEFINITION AGENCOURT_8102304 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6252811
5', mRNA sequence.
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VERSION BUI74317.1 GI:22688301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM2399 row: k column: 20
High quality sequence stop: 587.
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
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10 CGAGGACTGCTCGAGGTGGAGAACTGCACCCAGCTGGGGGAGCAGTGTGGACCGCGG 69
Qy 61 CATCCGCGAGTTGGCTCTCTGACCGTCATCAGCAAGGTCAGCTTGAAGTGGTGA 120
Db |||||
70 CATCCGCGAGTTGGCTCTCTGACCGTCATCAGCAAGGTCAGCTTGAAGTGGTGA 129
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Db |||||
130 TGACTCACAGGACTACTAGCTGGGCAAGAGAACATCAGTGTGTGACACCGACTTTGTG 189
Qy 181 CAACGGCAGCGGGGCCATGCCCTGACGGGTCGCCGATCCCTGCGCTGCCCTGC 240
Db |||||
190 CAACGGCAGCGGGGCCATGCCCTGACGGGTCGCCGATCCCTGCGCTGCCCTGC 249
Qy 241 ACTCGGCTGCTCTCTGGGACCC 265
Db |||||
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Test

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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(without alignments)
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Perfect score: 230
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Scoring table: IDENTITY NUC
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Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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32: em_hvg_other:
33: em_hvg_mus:
34: em_hvg_pln:
35: em_hvg_rod:
36: em_hvg_man:
37: em_hvg_vrt:
38: em_sy:
39: em_hvg_hum:
40: em_hvg_mus:
41: em_hvg_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	230	100.0	946	9	HS297436	Hom sapi
5	230	100.0	960	6	AR410610	Sequence
6	230	100.0	960	6	AX201328	Sequence
7	230	100.0	960	6	AX697426	Sequence
8	230	100.0	960	6	BD075381	Secretory
9	230	100.0	960	6	BD172241	Secreted
10	230	100.0	960	6	BD172560	Secreted
11	230	100.0	960	6	BD172879	Secreted
12	230	100.0	960	6	BD173198	Secreted
13	230	100.0	960	6	BD175232	Secretory
14	230	100.0	960	9	AY358912	Hom sapi
15	230	100.0	979	6	BD076397	Human pro
16	230	100.0	1015	9	EC023582	Hom sapi
17	230	100.0	157839	2	AC015718	Hom sapi
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19	223.6	97.2	103247	2	AF176678	Hom sapi
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21	217.4	94.5	990	6	AX014204	Sequence
22	217.4	94.5	990	6	BD205072	Human nuc
23	217.4	94.5	990	9	AF043498	Hom sapi
24	217.4	94.5	998	6	AR162849	Sequence
25	217.4	94.5	998	6	BD264314	PSCA: pro
26	217.4	94.5	998	6	AR302232	Sequence
27	217.4	94.5	998	6	AX080304	Sequence
28	217.4	94.5	998	6	BD193367	Prostate
29	191.4	83.2	494	6	AR026974	Sequence
30	158.6	69.0	251	6	AR026989	Sequence
31	118	51.3	372	6	AX155553	Sequence
32	115	50.0	369	6	BD076387	Human pro
33	101	43.9	372	6	AX155569	Sequence
34	97.8	42.5	372	6	AX155567	Sequence
35	77	33.5	77	6	AR026993	Sequence
36	64.4	28.0	441	6	AR162850	Sequence
37	64.4	28.0	441	6	AR302233	Sequence
38	64.4	28.0	441	6	AX080306	Sequence
39	64.4	28.0	441	6	BD193368	Prostate
40	61	26.5	864	10	AF319173	Mus muscu
41	61	26.5	190653	10	AC118022	Mus muscu
42	54.2	23.6	228208	2	AC119786	Rattus no
43	54.2	23.6	252914	2	AC097431	Rattus no
44	51.8	22.5	286	6	AR026988	Sequence
45	42.4	18.4	692	6	AX868894	Sequence

ALIGNMENTS

RESULT 1
AR026991
LOCUS AR026991 230 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5856136.
ACCESSION AR026991
VERSION AR026991.1 GI:5937831
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 230)
AUTHORS Au-Young,J.
TITLE Human stem cell antigens
JOURNAL Patent: US 5856136-A 24 05-JAN-1999;
FEATURES Location/Qualifiers

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source          1. .230
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 230; DB 6; Length 230;
Best Local Similarity 100.0%; Pred. No. 5e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCGAGCGGGGCCCATGCTTGCAGCGCGGTGCGGC 60
Db 1 GTGCTGTGACACCGACTTGTGCAACGCGAGCGGGGCCCATGCTTGCAGCGCGGTGCGGC 60

QY 61 CATCCTTGGCGTCTCCCTGCACTCGGCTGCTGCTTGGGGAACCGGCGAGCTATAGGC 120
Db 61 CATCCTTGGCGTCTCCCTGCACTCGGCTGCTGCTTGGGGAACCGGCGAGCTATAGGC 120

QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGGTGCCTCCAGGCGCTCTGTGCCACTCC 180
Db 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGGTGGTGCCTCCAGGCGCTCTGTGCCACTCC 180

QY 181 TCACAGACCTGGCCAGTGGAGCGCTTCTGTTCTTCTGAGGCACATCCT 230
Db 181 TCACAGACCTGGCCAGTGGAGCGCTTCTGTTCTTCTGAGGCACATCCT 230

RESULT 2
LOCUS          AX014148          758 bp          DNA          linear          PAT 07-SEP-2000
DEFINITION     Sequence 16 from Patent WO9954447.
ACCESSION      AX014148
VERSION        AX014148.1 GI:10040595
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1. Human nucleic acid sequences of bladder tumour tissue
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Schmitt,A., Specht,T., Dahl,B., Hinzmann,B., Rosenthal,A. and
              Pilarsky,C.
              Human nucleic acid sequences of bladder tumour tissue
              Patent: WO 9954447-A 16 28-OCT-1999;
              SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
              BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
              (DE); PILARSKY CHRISTIAN (DE)
FEATURES       Location/Qualifiers
source         1. .758
/organism="Homo sapiens"
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ORIGIN

Query Match      100.0%; Score 230; DB 6; Length 758;
Best Local Similarity 100.0%; Pred. No. 3.5e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCGAGCGGGGCCCATGCTTGCAGCGCGGTGCGGC 60
Db 37 GTGCTGTGACACCGACTTGTGCAACGCGAGCGGGGCCCATGCTTGCAGCGCGGTGCGGC 96

QY 61 CATCCTTGGCGTCTCCCTGCACTCGGCTGCTGCTTGGGGAACCGGCGAGCTATAGGC 120
Db 61 CATCCTTGGCGTCTCCCTGCACTCGGCTGCTGCTTGGGGAACCGGCGAGCTATAGGC 156

QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGGTGGTGCCTCCAGGCGCTCTGTGCCACTCC 180
Db 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGGTGGTGGTGCCTCCAGGCGCTCTGTGCCACTCC 216

QY 181 TCACAGACCTGGCCAGTGGAGCGCTTCTGTTCTTCTGAGGCACATCCT 230
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ORIGIN

Query Match      100.0%; Score 230; DB 6; Length 758;
Best Local Similarity 100.0%; Pred. No. 3.5e-33;
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QY 1 GTGCTGTGACACCGACTTGTGCAACGCGAGCGGGGCCCATGCTTGCAGCGCGGTGCGGC 60
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QY 61 CATCCTTGGCGTCTCCCTGCACTCGGCTGCTGCTTGGGGAACCGGCGAGCTATAGGC 120
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QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGGTGGTGCCTCCAGGCGCTCTGTGCCACTCC 180
Db 157 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGGTGGTGGTGCCTCCAGGCGCTCTGTGCCACTCC 216

QY 181 TCACAGACCTGGCCAGTGGAGCGCTTCTGTTCTTCTGAGGCACATCCT 230
Db 217 TCACAGACCTGGCCAGTGGAGCGCTTCTGTTCTTCTGAGGCACATCCT 266

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RESULT 3
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LOCUS          BD205056          758 bp          DNA          linear          PAT 17-JUL-2003
DEFINITION     Human nucleic acid sequence originating in cystic cancer tissue.
ACCESSION      BD205056
VERSION        BD205056.1 GI:33014826
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,B. and
              Rosenthal,A.
              Human nucleic acid sequence originating in cystic cancer tissue
              Patent: JP 2002512023-A 10 23-APR-2002;
              METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
              OS Homo sapiens (human)
              PN JP 2002512023-A/10
              PD 23-APR-2002
              PF 15-APR-1999 JP 2000544779
              PR 21-APR-1998 DE 198 18 619 3
              PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
              PI EDGAR DAHL,
              PI ANDRE ROSENTHAL
              PC C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P13/10,
              PC A61P35/00,
              PC C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12P21/08,C12Q1/68, PC
              C12N15/00,
              CC A61K37/02,C12N5/00
              CC Human nucleic acid sequence originating in cystic cancer CC
FEATURES       Location/Qualifiers
FT source      1. .758
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Query Match      100.0%; Score 230; DB 6; Length 758;
Best Local Similarity 100.0%; Pred. No. 3.5e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCGAGCGGGGCCCATGCTTGCAGCGCGGTGCGGC 60
Db 37 GTGCTGTGACACCGACTTGTGCAACGCGAGCGGGGCCCATGCTTGCAGCGCGGTGCGGC 96

QY 61 CATCCTTGGCGTCTCCCTGCACTCGGCTGCTGCTTGGGGAACCGGCGAGCTATAGGC 120
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QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGGTGGTGCCTCCAGGCGCTCTGTGCCACTCC 180
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QY 181 TCACAGACCTGGCCAGTGGAGCGCTTCTGTTCTTCTGAGGCACATCCT 230
Db 217 TCACAGACCTGGCCAGTGGAGCGCTTCTGTTCTTCTGAGGCACATCCT 266

RESULT 4
HSA297436
LOCUS          HSA297436          946 bp          mRNA          linear          PRI 13-OCT-2000
DEFINITION     Homo sapiens mRNA for prostate stem cell antigen (PSCA gene).
ACCESSION      HSA297436
VERSION        HSA297436.1 GI:9367211
KEYWORDS       prostate stem cell antigen; PSCA gene.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Bahrenberg, G., Brauers, A., Joost, H.G. and Jakse, G.
JOURNAL Reduced expression of PSA, a member of the LY-6 family of cell
MEDLINE surface antigens, in bladder, esophagus, and stomach tumors
20431743 Biochem. Biophys. Res. Commun. 275 (3), 783-788 (2000)
PUBMED
REFERENCE 2 (bases 1 to 946)
AUTHORS Bahrenberg, G.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2000) Bahrenberg G., Institut fuer Pharmakologie
und Toxikologie, RWTH Aachen, Wendlingweg2, Aachen, NRW, 52057,
GERMANY

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/country="Germany"
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/gene="PSCA"
CDS 20..391
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QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCGAGCGGCTGCCGC 60
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QY 61 CATCCTTGGCGTCTCCCTGCACTGGCTGCTGCTGGGACCGGCGCAGCTATAGGC 120
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QY 121 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTGGCCCGAGGCTCTGTGCCACTCC 180
Db 394 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTGGCCCGAGGCTCTGTGCCACTCC 453
QY 181 TCACAGACTGGCCCGCAGTGGAGCGCTGCTGGTTCCTGAGGCAATCTCT 230
Db 454 TCACAGACTGGCCCGCAGTGGAGCGCTGCTGGTTCCTGAGGCAATCTCT 503

RESULT 5
LOCUS AR410610
DEFINITION Sequence 17 from patent US 6635468.
ACCESSION AR410610
VERSION AR410610.1 GI:40162110
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 960)

AUTHORS Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
Fliviaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,
Kijavini, I.J., Mathers, J.P., Pan, J., Paoni, N.F., Roy, M.A.,
Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6635468-A 17 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..960
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Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCGAGCGGCTGCCGC 60
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Db 304 CATCCTTGGCGTCTCCCTGCACTGGCTGCTGCTGGGACCGGCGCAGCTATAGGC 363
QY 121 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTGGCCCGAGGCTCTGTGCCACTCC 180
Db 364 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTGGCCCGAGGCTCTGTGCCACTCC 423
QY 181 TCACAGACTGGCCCGCAGTGGAGCGCTCTCTGGTTCCTGAGGCAATCTCT 230
Db 424 TCACAGACTGGCCCGCAGTGGAGCGCTCTCTGGTTCCTGAGGCAATCTCT 473

RESULT 6
LOCUS AX201328
DEFINITION Sequence 7 from Patent WO0153486.
ACCESSION AX201328
VERSION AX201328.1 GI:151391156
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,
Hillan, K.J., Mathers, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V.,
Stoner, D.W., Watanabe, C.K. and Wood, W.I.
TITLE Compositions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 7 26-JUL-2001;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 230; DB 6; Length 960;
Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CATCCTTGGCGTCTCCCTGCACTGGCTGCTGCTGGGACCGGCGCAGCTATAGGC 120
Db 304 CATCCTTGGCGTCTCCCTGCACTGGCTGCTGCTGGGACCGGCGCAGCTATAGGC 363
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BD172241
LOCUS
DEFINITION
SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
THE SAME.
BD172241
ACCESSION
BD172241.1 GI:28413539
KEYWORDS
JP 200223786-A/14.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 960)
AUTHORS
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE
SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
THE SAME
JOURNAL
PATENT: JP 200223786-A 14 13-AUG-2002;
GENENTECH INC
COMMENT
OS Homo sapiens (human)
PN JP 200223786-A/14
PD 13-AUG-2002
PF 18-DEC-2001 JP 2001385135
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
18-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
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17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065563 PR
21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR
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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC
C12P21/02, C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC
(C12P21/02, C12R1:645), C12N15/00, C12N5/00
CC SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS
ENCODING THE SAME
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source 1..960
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/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred No. 3, 2e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCTCGCGCGGCTGCGGC 60
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Db 304 CATCTTTCGGCTGTCTCCTGCACTCGGCGCTGCTCTCTGGGACCCGCGCAGCTATAGGC 363
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Db 364 TCTGGGGGGCCCCCTGTCAGCCACACACTGGGTGTGGTGGCCAGGCTCTGTGCACTCC 423
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QY 181 TCACAGACCTGGCCAGTGGGAGGCTGTCTGTGGTCTCTGAGGCAATCCT 230
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BD172560
LOCUS
DEFINITION
SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
THE SAME.
BD172560
ACCESSION
BD172560.1 GI:28413862
KEYWORDS
JP 2002238586-A/14.
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 960)
AUTHORS
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE
SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
THE SAME
JOURNAL
PATENT: JP 2002238586-A 14 17-AUG-2002;
GENENTECH INC
COMMENT
OS Homo sapiens (human)
PN JP 2002238586-A/14
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385205
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR
31-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/064248 PR
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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC
C12P21/02, C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC
(C12P21/02, C12R1:645), C12N15/00, C12N5/00
CC SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS
ENCODING THE SAME
FH Key Location/Qualifiers
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FT /organism="Homo sapiens (human)"
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/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 230; DB 6; Length 960;
Best Local Similarity 100.0%; Pred No. 3, 2e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCTCGCGCGGCTGCGGC 60
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24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PR
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K16/435,C07K16/18,C07K19/00,C12N1/19,C12N1/21,PC
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encoding the same
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Best Local Similarity 100.0%; Pred. No. 3.2e-33;
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QY 61 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGGCACTATAGGC 120
DB 304 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGGCACTATAGGC 363
QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGTGGCCAGGCTGTGGCCACATCC 180
DB 364 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGTGGCCAGGCTGTGGCCACATCC 423
QY 181 TCACAGACTTGGCCCACTGGAGCCCTGTCTCTGCTTCTGAGGCACATCTT 230
DB 424 TCACAGACTTGGCCCACTGGAGCCCTGTCTCTGCTTCTGAGGCACATCTT 473

RESULT 13
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LOCUS 960 bp DNA linear PAT 18-MAR-2003
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding
the same.
ACCESSION BD175232
VERSION BD175232.1 GI:29120928
KEYWORDS JP 2002253280-A/14.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Caciarrhini; Homnidae; Homo.
1 (Bases 1 to 960)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secretory and transmembrane polypeptide and nucleic acid encoding
the same
JOURNAL Patent: JP 2002253280-A 14 10-SEP-2002;
GENETECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002253280-A/14
PD 10-SEP-2002
PF 18-DEC-2001 JP 2001385319
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PR
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06,PC
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PC C12P21/08,(C12N1/19,C12R1/645),(C12N1/21,C12R1/19),C12N5/10,
PC C12R1/91),
PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1/91) CC
Secretory and transmembrane polypeptide and nucleic acid CC
encoding the same
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FT source 1..960
PI Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCGGCTGCCGC 60
DB 244 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCGGCTGCCGC 303
QY 61 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGGCACTATAGGC 120
DB 304 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGGCACTATAGGC 363
QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGTGGCCAGGCTGTGGCCACATCC 180
DB 364 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGTGGCCAGGCTGTGGCCACATCC 423
QY 181 TCACAGACTTGGCCCACTGGAGCCCTGTCTCTGCTTCTGAGGCACATCTT 230
DB 424 TCACAGACTTGGCCCACTGGAGCCCTGTCTCTGCTTCTGAGGCACATCTT 473

RESULT 13
BD175232
LOCUS 960 bp DNA linear PAT 18-MAR-2003
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding
the same.
ACCESSION BD175232
VERSION BD175232.1 GI:29120928
KEYWORDS JP 2002253280-A/14.
SOURCE Homo sapiens (human)

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Db		
121	TCTGGGGGGCCCCCTGCAGCCACACACTGGGTTGGTGGCCAGGCGCTGTGGCACTCC	180
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Db		
181	TCACAGACTCTGGCCCACTGGGAGCGCTCTCTGGTTCTCTGAGGCACATCCT	230
Qy		
424	TCACAGACTCTGGCCCACTGGGAGCGCTCTCTGGTTCTCTGAGGCACATCCT	473
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LOCUS	AY358912				
DEFINITION	Homio sapiens clone DNA34435 prostate stem cell A (U0206) mRNA,				
	partial cds.				
ACCESSION	AY358912	1	GI:37182941		
KEYWORDS	FLI_CDNA				
SOURCE	Homio sapiens (human)				
ORGANISM	Homio sapiens				
REFERENCE	1 (bases 1 to 960)				
AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Marx,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,D., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wiand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.				
TITLE	The Secreted Protein Discovery Initiative (SPDI), a large-scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment				
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)				
PUBMED	12975309				
REFERENCE	2 (bases 1 to 960)				
AUTHORS	Clark,H.F.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Wav. South San Francisco, CA 94080, USA				

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Db	364	TCTGGGGGGCCCCGCTGTGAGGCCACCACTGTGGTGTGGTGTCCGCCAGGCTCTGTGGCACTCC	423
Qy	181	TCAGACACCTTGGCCCCAGTCGGGAGCGCTGTCTGTGGTTCCTGTGAGGCACATCCT	230
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RESULT 15	BD076397	979 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD076397				
DEFINITION	Human protein having transmembrane domain and DNA encoding the same.				
ACCESSION	BD076397				
VERSION	BD076397.1	GI:22622000			
KEYWORDS	JP 2001519154-A/11.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 979)				
TITLE	Kato, S., Kimura, T., Sekine, S. and Kobayashi, M.				
JOURNAL	Human protein having transmembrane domain and DNA encoding the same				
COMMENT	Patent: JP 2001519154-A 11 23-OCT-2001;				
	SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC				
	OS Homo sapiens (human)				
	PN JP 2001519154-A/11				

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Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61  CATCTTTCGGCTGTCTCCTGCACATCGGCTCTGCTCTGTGGACCCGGCGAGCTATAGGC 120
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Job time : 1152.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 04:33:41 ; Search time 150.354 Seconds
(without alignments)
6498.587 Million cell updates/sec

Title: US-09-079-874-6

Perfect score: 230

Sequence: 1 GFGCTGTGACACCGACTGTG.....TGGTTCCTGAGGCACATCCT 230

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	230	100.0	960	2	Aax52217 Protein P
6	230	100.0	960	3	Adc78337 Human PRO
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Adc28749 Human sec	41	230	100.0	960	9	ADC28749
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Adc19291 Human sec	43	230	100.0	960	9	ADC19291
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Adc12809 Human sec	45	230	100.0	960	9	ADC12809

ALIGNMENTS

RESULT 1
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ID AAV38062 standard; cDNA; 230 BP.
XX
AC AAV38062;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human stem cell antigen 2 partial sequence from Incyte clone 1314679.
XX
KW Human; stem cell antigen; SCAH-1; SCAH-2; THP-1; bladder tumour;
KW diagnosis; screening; sca-2; LY-6 family; leukaemia; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9800540-A1.
XX
PD 08-JAN-1998.
XX
PF 25-JUN-1997; 97WO-US010956.
XX
PR 03-JUL-1996; 96US-00675508.
XX (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J;
XX
DR WPI; 1998-427478/36.
XX
PT Human stem cell antigens, SCAH-1 and SCAH-2 - useful to, e.g. diagnose
PT and treat SCAH-1 or SCAH-2 related conditions such as tumours and screen
PT inhibitory compounds.
XX
PS Disclosure; Page 50; 66pp; English.
XX
CC The present sequence represents an Incyte clone used in the determination
CC of human stem cell antigen 2 (SCAH-2). SCAH proteins can be administered
CC therapeutically, e.g. to inhibit or reverse the development of tumours.
CC Antibodies to SCAH proteins can be used in diagnostic tests for
CC conditions associated with protein expression in biological samples, by
CC combining a sample with the antibody under conditions suitable for
CC antibody binding to the protein to form a complex, and detecting the
CC complex. Antibodies to SCAH-2 are especially useful in diagnostic tests
CC for conditions/diseases such as leukaemias or malignant local tumours
CC associated with SCAH-2 expression. SCAH-1 and SCAH-2 have homology to sca
CC -2 and other stem cell antigens, and have characteristics of the LY-6

CC family of cysteine rich proteins. The functional similarities among LY-6
CC family proteins previously reported, and the expression of SCAH-1 and
CC SCAH-2 in tumours from several tissues (e.g. breast, lung, bladder)
CC indicated that SCAH proteins may be useful as anticancer agents, SCAH
CC antibodies, antagonists or inhibitors identified using the proteins could
CC also be useful in anticancer treatments and to intervene in all responses
CC associated with transplant rejection and autoimmune diseases e.g. lupus
CC nephritis. The nucleic acid sequences encoding SCAH proteins are also
CC useful therapeutically to treat, e.g. leukaemias and cancers of the
CC bladder or breast
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Best Local Similarity 100.0%; Pred. No. 3.9e-42;
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QY 121 TCTGGGGGCGCCCGCTGCGAGCCACACTGGGTGTGGTGTGCGCCAGCGCTTGTGCCACTCC 180
DB 121 TCTGGGGGCGCCCGCTGCGAGCCACACTGGGTGTGGTGTGCGCCAGCGCTTGTGCCACTCC 180
QY 181 TCACAGACCTGCCCAGTGGGAGCCTGCTGCTGTTCTTCTGAGGCACATCCT 230
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RESULT 2
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XX
AC AAV80391;
XX
DT 23-FEB-1999 (first entry)
XX
DE Nucleotide sequence of Utl16 gene-specific clone 1314679.
XX
XX Utl16; urinary tract; epitope; antigen; detection; diagnosing;
KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
KW metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO9851824-A1.
XX
XX 19-NOV-1998.
XX
XX 15-MAY-1998; 98WO-US009972.
XX
XX 15-MAY-1997; 97US-00856652.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
PI Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
PI Stroupe SD;
XX
XX WPI; 1999-045237/04.
XX
XX New method for detecting diseases of the urinary tract - comprises use of
PT a Utl16 polynucleotide, protein or antibodies, used for preventing and
PT treating urinary tract infections and cancer.
XX
XX Claim 1; Fig 1A-C; 113pp; English.
XX
XX Sequences AAV80386 to AAV80396 represent partially overlapping nucleotide

CC sequences of the Utl16 gene-specific clones derived from urinary tract
CC tissue. The invention relates to a method of detecting the presence of a
CC target Utl16 polynucleotide in a test sample using these Utl16-specific
CC sequences. Host cells transfected with an expression vector containing
CC the Utl16 gene can be used to produce a Utl16 polypeptide recombinantly.
CC This polypeptide has at least one Utl16 epitope which can be used in a
CC method for detecting Utl16 antigen in a test sample. The polynucleotides
CC and polypeptides are useful for detecting, diagnosing, monitoring,
CC staging, prognosticating, in vivo imaging, preventing, treating or
CC determining the predisposition of a subject to diseases and conditions of
CC the urinary tract, such as urinary tract cancer. Antibodies specifically
CC binding to an epitope of Utl16 antigen, and agonists are useful for
CC treating urinary tract diseases, tumours and metastases
XX
SQ Sequence 230 BP; 27 A; 88 C; 71 G; 44 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.9e-42;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACACGACTTGTGCAAGCCAGCGGGGCCCATGCTGCGAGCGGCTGCGGC 60
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DB 121 TCTGGGGGCGCCCGCTGCGAGCCACACTGGGTGTGGTGTGCGCCAGCGCTTGTGCCACTCC 180
QY 181 TCACAGACCTGCCCAGTGGGAGCCTGCTGCTGTTCTTCTGAGGCACATCCT 230
DB 181 TCACAGACCTGCCCAGTGGGAGCCTGCTGCTGTTCTTCTGAGGCACATCCT 230

RESULT 3
AAV68608
ID AAV68608 standard; cDNA; 230 BP.
XX
AC AAV68608;
XX
DT 16-MAR-1999 (first entry)
XX
XX Human PS116 EST clone 1314679.
DE
XX Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
KW detection; therapy; prostate cancer; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO9851805-A1.
XX
XX 19-NOV-1998.
XX
XX 15-MAY-1998; 98WO-US010041.
XX
XX 15-MAY-1997; 97US-00856653.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
XX WPI; 1999-045234/04.
XX
XX New method for detecting diseases of the prostate - comprises use of a
PT PS116 polynucleotide, protein or antibodies, useful for preventing and
PT treating prostate infections and cancer.
XX
XX Claim 1; Page 92; 118pp; English.

XX This sequence represents an expressed sequence tag (EST) clone of the
 CC PS116 gene isolated from a human prostate tissue library. This sequence
 CC can be used in the method of the invention for detecting a target PS116
 CC polynucleotide (PN), that comprises: contacting a sample with at least 1
 CC PS116-specific PN or complement; and detecting the target PS116 PN, where
 CC the specific PN has at least 50% identity with this sequence. The PNs,
 CC PS116 polypeptides or PS116 amplicons are used to detect prostate
 CC disease. Antibodies (Abs) against PS116 are used in assay kits to detect
 CC PS116 antigen or anti-PS116 Ab, and the Abs are preferably attached to a
 CC solid phase. The polypeptides are used for detecting PS116-specific Abs
 CC in a sample, and for producing Abs after immunising a subject. Plasmids
 CC encoding PS116 epitopes can also be administered to a subject to obtain
 CC Abs. The cDNAs and polypeptides are useful for detecting, diagnosing,
 CC staging, monitoring, prognosticating, in vivo imaging, preventing,
 CC treating or determining the predisposition of a subject to diseases and
 CC conditions of the prostate, such as prostate cancer. The Abs and agonists
 CC or inhibitors are useful for treating prostate diseases, tumours and
 CC metastases
 XX
 SQ Sequence 230 BP; 27 A; 88 C; 71 G; 44 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 3.9e-42;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 60
 Db 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 60
 QY 61 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTCTGGGACCGCGCAGCTATAGGC 120
 Db 61 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTCTGGGACCGCGCAGCTATAGGC 120
 QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGGCCCGAGCCCTGTGGCACTCC 180
 Db 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGGCCCGAGCCCTGTGGCACTCC 180
 QY 181 TCACAGACTGGCCCGAGTGGAGCCCTGTCTGGTTCTCTGAGGCACATCTT 230
 Db 181 TCACAGACTGGCCCGAGTGGAGCCCTGTCTGGTTCTCTGAGGCACATCTT 230

RESULT 4
 AAZ24404
 ID AAZ24404 standard; cDNA; 758 BP.
 XX
 AC AAZ24404;
 XX
 DT 14-FEB-2000 (first entry)
 XX

DE Human bladder tumour cDNA library derived EST 16.

XX Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
 KW treatment; gene therapy; EST; ss.
 XX

OS Homo sapiens.

XX DE19918619-A1.

PN 28-OCT-1999.

XX 21-APR-1998; 98DE-01018619.

XX 21-APR-1998; 98DE-01018619.

XX (META-) METAGEN GES GENOMFORSCHUNG MRH.

PA Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 PI WPI; 1999-612028/53.

DR WPI; 1999-612028/53.

XX New nucleic acid sequences expressed in bladder tumor tissue, and derived

PT polypeptides, for treatment of bladder tumor and identification of
 PT therapeutic agents.

XX Claim 3; Page 72; 132pp; German.

XX This invention describes novel polypeptide fragments (I) and the
 CC polynucleotides (II) that encode them that are highly expressed in a
 CC human bladder tumor and which have cytostatic activity. (II) are used
 CC for recombinant expression of (I) and to isolate complete genes. (I) are
 CC used to identify agents suitable for treatment of bladder cancer, to
 CC directly treat this form of cancer (including expression from gene
 CC therapy vectors) or are used in a preparation for cancer treatment. (I)
 CC is also used for the generation of specific antibodies. (II) are
 CC identified by assembling ESTs (expressed sequence tags) from a particular
 CC tissue type before comparison of expression patterns. This allows a
 CC significantly longer fragment of the gene to be revealed, and therefore
 CC reduces the number of failures associated with the fact that ESTs from
 CC different libraries may represent different parts of the same unknown
 CC gene, distorting the estimated frequency of occurrence in a particular
 CC tissue. AAZ43260-243309 represent expressed sequence tag (EST) fragments
 CC isolated from a human bladder tumour cDNA library which encode the
 CC proteins represented in AAZ66143-Y66198

XX SQ Sequence 758 BP; 147 A; 261 C; 212 G; 138 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 2; Length 758;
 Best Local Similarity 100.0%; Pred. No. 4.1e-42;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 60
 Db 37 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 96
 QY 61 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTCTGGGACCGCGCAGCTATAGGC 120
 Db 97 CATCTTGGCTGCTCCCTGCACTCGGCTGTGCTCTGGGACCGCGCAGCTATAGGC 156
 QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGGCCCGAGCCCTGTGGCACTCC 180
 Db 157 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGGCCCGAGCCCTGTGGCACTCC 216
 QY 181 TCACAGACTGGCCCGAGTGGAGCCCTGTCTGGTTCTCTGAGGCACATCTT 230
 Db 217 TCACAGACTGGCCCGAGTGGAGCCCTGTCTGGTTCTCTGAGGCACATCTT 266

RESULT 5

AAZ52217

ID AAZ52217 standard; DNA; 960 BP.

XX AC AAZ52217;

XX 25-JUN-1999 (first entry)

XX Protein PRO232 cDNA clone DNA34435-1140.

XX Secreted protein; transmembrane protein; human; enterocolitis;

XX Zollinger-Ellison syndrome; gastrointestinal ulceration;

XX congenital microvillus atrophy; skin disease; cell growth;

XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;

XX dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;

XX wound healing; tissue repair; ss.

XX Homo sapiens.

XX WO9914328-A2.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-00591115P.
 PR 17-SEP-1997; 97US-00591117P.
 PR 17-SEP-1997; 97US-00591119P.
 PR 17-SEP-1997; 97US-00591121P.
 PR 17-SEP-1997; 97US-00591123P.
 PR 17-SEP-1997; 97US-00591124P.
 PR 17-SEP-1997; 97US-00591126P.
 PR 18-SEP-1997; 97US-00592631P.
 PR 18-SEP-1997; 97US-00592632P.
 PR 15-OCT-1997; 97US-00621256P.
 PR 15-OCT-1997; 97US-00621257P.
 PR 17-OCT-1997; 97US-00622857P.
 PR 17-OCT-1997; 97US-00622858P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062815P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063545P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-00655846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 PA (GETH) GENENTECH INC.
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 DR WPI; 1999-229533/19.
 DR P-PSDB; AAY13347.
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 FT gastrointestinal ulceration.
 XX Claim 2; Fig 8; 320pp; English.
 XX
 CC AX52213-74 encode secreted and transmembrane human proteins, and are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides have
 CC specific uses based on their homology to known polypeptides, e.g. PRO211
 CC and PRO217 can be used for disorders associated with the preservation and
 CC maintenance of gastrointestinal mucosa and the repair of acute and
 CC chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,
 CC gastrointestinal ulceration and congenital microvillus atrophy), skin
 CC diseases associated with abnormal keratinocyte differentiation (e.g.
 CC psoriasis, epithelial cancers such as lung squamous cell carcinoma of the
 CC vulva and gliomas), potent effects on cell growth and development,
 CC

CC diseases related to growth or survival of nerve cells including
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.
 CC PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX
 SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;
 Query Match 100.0%; Score 230; DB 2; Length 960;
 Best Local Similarity 100.0%; Pred. No. 4.2e-42;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGACGCGGTGCGGC 60
 DB 244 GTCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGACGCGGTGCGGC 303
 QY 61 CATCCTTGGCGTCTCCCTGCACTGGGCTGTGCTCTGGGGACCCCGGCCAGCTATAGGC 120
 DB 304 CATCCTTGGCGTCTCCCTGCACTGGGCTGTGCTCTGGGGACCCCGGCCAGCTATAGGC 363
 QY 121 TGTGGGGGGCCCGGTGACAGCCACACTGGGTGGTGGCCCGCCAGGCTCTGTGCACTCC 180
 DB 364 TGTGGGGGGCCCGGTGACAGCCACACTGGGTGGTGGCCCGCCAGGCTCTGTGCACTCC 423
 QY 181 TCACAGACCTGGCCCGCAGTGGGAGCCTGCTGTTCTCTGAGGCACATCCT 230
 DB 424 TCACAGACCTGGCCCGCAGTGGGAGCCTGCTGTTCTCTGAGGCACATCCT 473
 RESULT 6
 ADC78337
 ID ADC78337 standard; cDNA; 960 BP.
 AC ADC78337;
 XX
 DT 01-JAN-2004 (first entry)
 XX Human PRO232 cDNA.
 XX
 KW antiinflammatory; antitumor; cytostatic; antipruritic; antiparkinsonian;
 KW neurotrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
 XX Homo sapiens.
 OS
 XX
 XX WO200015795-A2.
 XX
 XX 23-MAR-2000.
 XX
 XX 15-SEP-1999; 99WO-US021090.
 XX
 XX 16-SEP-1998; 98WO-US019330.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 XX Yuan J;
 XX WPI; 2000-271434/23.
 XX P-PSDB; ADC78338.
 XX

PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT homology, e.g. to growth and cancer-associated antigens.
PS
XX Claim 2; SEQ ID NO 17; 355pp; English.

XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC The polypeptides and polynucleotides of the invention may be useful as
CC research tools and as therapeutics for treating enterocolitis, Zollinger-
CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC scarring and wound healing, nerve repair, thrombosis, bone and/or
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC infertility, premature aging, AIDS, diabetes complications and stroke.
CC The molecules may also be utilised during gene therapy procedures and
CC transgenic animal production. The current sequence is that of the human
CC PRO cDNA of the invention.

XX
SQ Sequence 960 BP; 182 A; 327 C; 274 G; 177 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 3; Length 960;

Best Local Similarity 100.0%; Pred. No. 4.2e-42;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCGGCTGCCGC 60
DB |||||
DB 244 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCGGCTGCCGC 303
QY 61 CATCCTTTGGCGTCTCCCTGCACCTGGCTGTCTGTGGGACCCGGCCAGCTATAGGC 120
DB |||||
DB 304 CATCCTTTGGCGTCTCCCTGCACCTGGCTGTCTGTGGGACCCGGCCAGCTATAGGC 363
QY 121 TCTGGGGGGCCCGCTGTGACGCCACACTGGGTGTGGTGTGCCCCAGGCTCTGTGCCACTCC 180
DB |||||
DB 364 TCTGGGGGGCCCGCTGTGACGCCACACTGGGTGTGGTGTGCCCCAGGCTCTGTGCCACTCC 423
QY 181 TCACAGACTTGGCCCGCTGTGAGCCCTGTCTGTCTTCTGAGGCACATCCT 230
DB |||||
DB 424 TCACAGACTTGGCCCGCTGTGAGCCCTGTCTGTCTTCTGAGGCACATCCT 473

RESULT 7

AAAF72375

ID AAF72375 standard; cDNA; 960 BP.

XX AAF72375;

AC AAF72375;

XX 24-APR-2001 (first entry)

DT 24-APR-2001 (first entry)

XX Human PRO232 cDNA.

DE Human PRO232 cDNA.

XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;

KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;

KW antiarthritic; antifertility; antidiabetic; antiviral; diabetes;

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;

KW ischaemia; inflammation; expressed sequence tag; EST; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US004414.

XX 07-JUL-1999; 99US-0143048P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IG;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX

DR WPI; 2001-081051/09.

XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).

XX Claim 2; Fig 8; 393pp; English.

PS The present sequence is an EST used to isolate one of sixty one nucleic
XX acids encoding novel secreted and transmembrane PRO polypeptides. The PRO
CC polypeptides are useful for treating skin diseases (e.g. psoriasis),
CC cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders
CC (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), wound repair, cardiovascular disorders
CC (e.g. endometrial bleeding angiogenesis, ischaemia such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), pigmentum. The PRO nucleic
CC acids have applications in molecular biology, including use as
CC hybridization probes, and in chromosome and gene mapping
XX

SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 4; Length 960;

Best Local Similarity 100.0%; Pred. No. 4.2e-42;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCGGCTGCCGC 60

DB |||||
DB 244 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCGGCTGCCGC 303

QY 61 CATCCTTTGGCGTCTCCCTGCACCTGGCTGTCTGTGGGACCCGGCCAGCTATAGGC 120

DB |||||
DB 304 CATCCTTTGGCGTCTCCCTGCACCTGGCTGTCTGTGGGACCCGGCCAGCTATAGGC 363

QY 121 TCTGGGGGGCCCGCTGTGACGCCACACTGGGTGTGGTGTGCCCCAGGCTCTGTGCCACTCC 180

DB |||||
DB 364 TCTGGGGGGCCCGCTGTGACGCCACACTGGGTGTGGTGTGCCCCAGGCTCTGTGCCACTCC 423

QY 181 TCACAGACTTGGCCCGCTGTGAGCCCTGTCTGTCTTCTGAGGCACATCCT 230

DB |||||
DB 424 TCACAGACTTGGCCCGCTGTGAGCCCTGTCTGTCTTCTGAGGCACATCCT 473

RESULT 8

ABK40257

ID ABK40257 standard; cDNA; 960 BP.

XX ABK40257;

AC ABK40257;

XX 15-JUL-2002 (first entry)

DT 15-JUL-2002 (first entry)

XX cDNA encoding human PRO232 polypeptide.

DE cDNA encoding human PRO232 polypeptide.

XX

PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066772P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Pilvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Faoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WJ;
DR WPI; 2003-361832/34.
DR P-PSDB; ABU71448.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
PT Generating antisense RNA and DNA, and in gene therapy.

XX Claim 2; Fig 8; 474pp; English.

XX The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides

CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays. The
CC present sequence encodes a human PRO polypeptide of the invention

XX Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 7; Length 960;

Best Local Similarity 100.0%; Pred. No. 4.2e-42;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGMAACCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCCGC 60

DB 244 GTGCTGTGACACCGACTTGTGCAACCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCCGC 303

QY 61 CATCCTTGGCTGCTCCCTGCACCTGGGCTGTGCTTCTGGGACCGGCCACGTATAGGC 120

DB 304 CATCCTTGGCTGCTCCCTGCACCTGGGCTGTGCTTCTGGGACCGGCCACGTATAGGC 363

QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGCTGTGCTTCTGGGACCGGCCACGTATAGGC 180

DB 364 TCTGGGGGGCCCGCTGCAGCCACACTGGGCTGTGCTTCTGGGACCGGCCACGTATAGGC 423

QY 181 TCACAGACCTGGCCAGTGGAGCCTGCTCTGGTCTCTGAGGCACATCCT 230

DB 424 TCACAGACCTGGCCAGTGGAGCCTGCTCTGGTCTCTGAGGCACATCCT 473

RESULT 11

ACA60013

ID ACA60013 standard; cDNA; 960 BP.

XX ACA60013;

XX DT 12-JUN-2003 (first entry)

XX Human cDNA for secreted/transmembrane protein PRO232.

XX Human; ss, gene; secreted protein; transmembrane protein; PRO;

XX Gene therapy; chromosome identification; chromosome marker.

XX Homo sapiens.

XX US2003003530-A1.

XX PD 02-JAN-2003.

XX 11-JUL-2001; 2001US-00904011.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059115P.

XX 17-SEP-1997; 97US-0059117P.

XX 17-SEP-1997; 97US-0059119P.

XX 17-SEP-1997; 97US-0059121P.

XX 17-SEP-1997; 97US-0059122P.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 15-OCT-1997; 97US-0062125P.

XX 17-OCT-1997; 97US-0062285P.

XX 21-OCT-1997; 97US-0062287P.

XX 24-OCT-1997; 97US-0062814P.

XX 24-OCT-1997; 97US-0062816P.

XX 24-OCT-1997; 97US-0063045P.

XX 24-OCT-1997; 97US-0063120P.

XX 24-OCT-1997; 97US-0063121P.

XX 24-OCT-1997; 97US-0063127P.

XX 24-OCT-1997; 97US-0063128P.

XX 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063341P.
PR 28-OCT-1997; 97US-0063342P.
PR 28-OCT-1997; 97US-0063344P.
PR 28-OCT-1997; 97US-0063349P.
PR 28-OCT-1997; 97US-0063350P.
PR 28-OCT-1997; 97US-0063356P.
PR 29-OCT-1997; 97US-0063343P.
PR 29-OCT-1997; 97US-0063370P.
PR 29-OCT-1997; 97US-0063372P.
PR 29-OCT-1997; 97US-0063373P.
PR 29-OCT-1997; 97US-0063375P.
PR 29-OCT-1997; 97US-0063373P.
PR 29-OCT-1997; 97US-0063374P.
PR 29-OCT-1997; 97US-0063378P.
PR 31-OCT-1997; 97US-0063370P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065186P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066772P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US011824.
PR 14-SEP-1998; 98WO-US011977.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 23-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini LJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-329602/31.
DR P-PSDB; ABU71894.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, in generating probes and in tissue typing.

XX Claim 2; Fig 8; 484pp; English.
XX
CC The invention relates to an isolated nucleic acid with at least 80%
CC nucleic acid sequence identity to a nucleotide sequence encoding one of
CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
CC PRO protein extracellular domain. Also included are a vector comprising
CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
CC polypeptide (by culturing the host cell for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture),
CC an isolated PRO polypeptide (having at least 80% sequence identity to:
CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
CC number (detailed in the specification); or (c) an extracellular domain of
CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
CC peptide), a chimeric molecule comprising a PRO polypeptide of fused to a
CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
CC modulating at least one biological activity of a cell expressing a PRO245
CC or PRO1868. Nucleic acids which encode PRO can be used to generate a PRO
CC transgenic animals or knock-out animals which may be used in the
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy, in chromosome identification, as
CC chromosome markers, or in generating probes. The PRO polypeptides are
CC useful as molecular markers for protein electrophoresis, and the isolated
CC nucleic acids may be used for recombinantly expressing those markers. The
CC PRO polypeptides and nucleic acids may also be used in tissue typing.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. The present sequence encodes a PRO protein
XX
SQ Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;
Query Match 100.0%; Score 230; DB 7; Length 960;
Best Local Similarity 100.0%; Pred. No. 4.2e-42;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACACCGACTTGTGCAACGCGCGGGCCATGCTGAGCGGCTGCGCG 60
DB 244 GTGCTGTGACACCGACTTGTGCAACGCGCGGGCCATGCTGAGCGGCTGCGCG 303
QY 61 CATCTTGGCGTGTCTCTGCACTGCGGCTGCTCTGCGGACCCGCGCAGCTATAGGC 120
DB 304 CATCTTGGCGTGTCTCTGCACTGCGGCTGCTCTGCGGACCCGCGCAGCTATAGGC 363
QY 121 TCTGGGGGGCCCGCTGCGACCCACACTGGGTGTGGTGGCCAGGCTCTGTGCCACTCC 180
DB 364 TCTGGGGGGCCCGCTGCGACCCACACTGGGTGTGGTGGCCAGGCTCTGTGCCACTCC 423
QY 181 TCACAGACCTGGCCAGTGGGAGCCTGTCTCTGTTCTCTGAGGCACATCCT 230
DB 424 TCACAGACCTGGCCAGTGGGAGCCTGTCTCTGTTCTCTGAGGCACATCCT 473
RESULT 12
ACD07413
ID ACD07413 standard; cDNA; 960 BP.
XX
XX ACD07413;
XX
XX DT 07-AUG-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO232 cDNA.
XX
XX KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
KW diagnostic; biosensor; bioreactor; Parkinson's disease;
KW Alzheimer's disease; inflammation; nephritis; wound healing;
KW nerve repair; collateral blood vessel formation; cancer;
KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
KW infertility; gene therapy; gene; ss.

```
XX OS Homo sapiens.
XX PN US2002197671-A1.
XX PD 26-DEC-2002.
XX PF 17-JUL-2001; 2001US-00907824.
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 29-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064805P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066770P.
XX 24-NOV-1997; 97US-0066772P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 01-DEC-1998; 98WO-US020594.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.

16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
26-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023228.
18-SEP-2000; 2000US-00665350.

(GETH ) GENENTECH INC.
Ashkenazi A, Botstein D, Desmoyers L, Eaton DL, Ferrara N;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen WE, Goddard A;
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;
WPI; 2003-370793/35.
P-PSDE; ABO01777.

New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
or strokes.

Claim 2; Fig 8; 482pp; English.

The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
Type Culture Collection (e.g. ATCC Deposit No. 209258) or a sequence
with at least 80% identity to a DNA encoding a PRO polypeptide comprising
any of 61 sequences having 164-1119 amino acids fully defined in the
specification. The PRO polypeptides or polynucleotides are useful as
pharmaceuticals, diagnostics, biosensors or bioreactors. These are
particularly useful for detecting or treating e.g. Parkinson's disease,
Alzheimer's disease, inflammations, nephritis, wound healing, nerve
repair, collateral blood vessel formation, cancers (e.g. colorectal
cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
ischemia, strokes, hypertension, heart attacks, atherosclerosis, or
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
therapeutic intervention in these diseases, and diagnostic determination
of the presence of these diseases. The PRO polypeptides are also useful
as molecular weight markers, or for chromosome identification. The PRO
genes are useful as hybridisation probes, or for screening libraries of
human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
therapy, particularly for replacing a defective gene. This sequence
encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 7; Length 960;
Best Local Similarity 100.0%; Pred. No. 4.2e-42;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACCGACTGTGTGACCGCGGGGCCCATGCGCGGTGCGGC 60
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 244 GTGCTGTGACCGACTGTGTGACCGCGGGGCCCATGCGCGGTGCGGC 303
| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 CATCTTGTGGCTGCTCCCTGTGACTCGGCTGTGCTGTGGGGACCCGCCAGCTATAGGC 120
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 304 CATCTTGTGGCTGCTCCCTGTGACTCGGCTGTGCTGTGGGGACCCGCCAGCTATAGGC 363
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QY 121 TGTGGGGGGCCCCGCTGTGACGCCACACTGGGTGTGGTGGTCCCGCCAGGCTCTGTGCGCACTCC 180
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Db 364 TCCTGGGGGGCCCGCTGCGCCACACACTGGGTGTGTGCTGCCAGGCTCTGTGCCACTCC 423
QY 181 TCACAGACTGGCCCGAGTGGAGCCCTGTCTCTGTTCTCTGAGGCACATCCT 230
Db 424 TCACAGACCTGGCCCGAGTGGAGCCCTGTCTCTGTTCTCTGAGGCACATCCT 473

RESULT 13
ABX71461
ID ABX71461 standard; cDNA; 960 BP.
XX AC ABX71461;
XX DT 10-MAR-2003 (first entry)
XX DE Human cDNA encoding secreted/transmembrane protein PRO232.
XX KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
KW gastrointestinal ulceration; skin disease; ss; gene;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; inflammatory disease;
KW rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
KW diabetic complication; wound repair.
XX OS Homo sapiens.
XX XX
XX US2002132240-A1.
XX PD 19-SEP-2002.
XX XX
XX 18-JUL-2001; 2001US-00909320.
XX XX
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059463P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
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XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
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XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063704P.
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XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 29-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
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PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065933P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030311.
PR 20-DEC-1999; 99WO-US030399.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH ) GENENTECH INC.
XX PA
XX ASkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PK, Wood WI;
XX WPI; 2003-147434/14.
DR P-PSDB; ABU54350.
XX
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
PT disease.
XX
XX Claim 2; Fig 8; 473pp; English.
XX
XX The invention relates to an isolated PRO polypeptide having at least 80%
CC amino acid sequence identity to: (a) any one of 61 fully defined amino
CC acid sequences given in the specification (appearing as ABU54347-
CC ABU54407); (b) an amino acid sequence encoded by the nucleotide sequence
CC deposited under American Type Culture Collection (accession numbers
CC listed in the specification); (c) any one of the PRO sequences which
CC lacks its associated signal peptide; (d) an extracellular domain of the
CC PRO polypeptide with its associated signal peptide; or (e) an
CC extracellular domain of the PRO polypeptide which lacks its associated
CC signal peptide. Also include are the nucleic acids encoding the PRO
CC polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
CC polypeptides and nucleic acids are useful in diagnosing or treating
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[illegible]

PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065833P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 20-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen WE, Goddard A;
PI Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PN, Wood WI;
XX
DR WPI: 2003-288105/28.
DR P-PSDB; ABU64502.
XX
PT New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245)
PT and genes encoding them, useful for detecting or treating e.g.
PT hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease
PT or inflammations.
XX
XX Claim 2; Fig 8; 477pp; English.
PS
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX and the nucleic acid encoding them. The polypeptides can be used to raise
XX antibodies that specifically bind to the PRO polypeptide, for linking a
XX bioactive molecule to a cell expressing a PRO protein and for modulating
XX at least one biological activity of a cell. The PRO polypeptides or
XX polynucleotides are also useful as pharmaceuticals, diagnostics,
XX biosensors or bioreactors, for detecting or treating e.g. hyperplasia,
XX endometriosis, cancers (e.g. those involving solid tumours), ischaemia,

CC coronary arterial disease, polycystic kidney disease, chronic or acute
CC renal failure, or inflammatory responses (e.g. asthma, rheumatoid
CC arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The sequences presented in ABX96017-ABX96378 are the genes
CC encoding, the primers amplifying and the probes detecting the PRO
CC polynucleotides of the invention

XX Sequence 960 BP; 182 A; 326 C; 274 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 230; DB 7; Length 960;

Best Local Similarity 100.0%; Pred. No. 4.2e-42;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGC 60

Db 244 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGC 303

Qy 61 CATCCTTTGCCCTGCTCCCTGCACTCGGCCCTGTGCTTCTGGGACCCGCCAGCTATAGGC 120

Db 304 CATCCTTTGCCCTGCTCCCTGCACTCGGCCCTGTGCTTCTGGGACCCGCCAGCTATAGGC 363

Qy 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGTGCTGCCAGGCTCTGTGCCACTCC 180

Db 364 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGTGCTGCCAGGCTCTGTGCCACTCC 423

Qy 181 TCACAGACCTGGGCCCACTGGGAGCCTGTCTGTTCTCTGAGGCACATCCT 230

Db 424 TCACAGACCTGGGCCCACTGGGAGCCTGTCTGTTCTCTGAGGCACATCCT 473

Search completed: September 18, 2004, 07:06:59

Job time : 150.354 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: September 18, 2004, 06:05:35 ; Search time 26.8697 Seconds
(without alignments)
4750.463 Million cell updates/sec

Title: US-09-079-874-6

Perfect score: 230

Sequence: 1 GTCGTGTGACACCGACTTGT.....TGGTTCCTGAGCACAATCCT 230

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

4: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

5: /cgn2_6/prodata/2/ina/PCUTS_COMB.seq:*

6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230	100.0	230	2	US-08-675-508-24
2	230	100.0	960	4	US-09-307-794A-17
3	230	100.0	960	4	US-09-305-125A-17
4	230	100.0	960	4	US-09-302-775A-17
5	217.4	94.5	998	3	US-09-203-939-1
6	217.4	94.5	998	3	US-09-251-835-1
7	217.4	94.5	998	3	US-09-318-503-1
8	217.4	94.5	998	3	US-09-038-261A-1
9	217.4	94.5	998	3	US-09-564-329A-1
10	191.4	83.2	494	2	US-08-675-508-4
11	158.6	69.0	251	2	US-08-675-508-22
12	77	33.5	77	2	US-08-675-508-26
13	64.4	28.0	441	3	US-08-203-939-3
14	64.4	28.0	441	3	US-09-251-835-3
15	64.4	28.0	441	3	US-09-318-503-3
16	64.4	28.0	441	3	US-09-038-261A-3
17	64.4	28.0	441	3	US-09-564-329A-3
18	51.8	22.5	286	2	US-08-675-508-21
19	38	16.5	2075	4	US-09-087-0315-2
20	38	16.5	2075	4	US-08-546-043-1
21	38	16.5	2075	4	US-09-514-885-2
22	37.6	16.3	819	4	US-09-252-991A-11082
23	37.6	16.3	2643	4	US-09-252-991A-11170
24	36.8	16.0	1907	4	US-09-399-913-5
25	36.8	16.0	1907	4	US-09-298-731-5
26	36.8	16.0	3053	4	US-09-252-991A-12299
27	36.8	16.0	3105	4	US-09-252-991A-12350

28	36.2	15.7	1037	4	US-09-461-325-90	Sequence 90, Appl
29	36.2	15.7	1037	4	US-10-012-542-90	Sequence 90, Appl
30	36.2	15.7	1268	4	US-09-461-325-126	Sequence 126, App
31	36.2	15.7	1268	4	US-10-012-542-126	Sequence 126, App
32	36	15.7	363	4	US-09-252-991A-3137	Sequence 3137, Ap
33	36	15.7	2310	4	US-09-252-991A-3040	Sequence 3040, Ap
34	35.8	15.6	1542	4	US-09-252-991A-4521	Sequence 4521, Ap
35	35.8	15.6	2592	4	US-09-252-991A-4250	Sequence 4250, Ap
36	35.8	15.6	3225	4	US-09-252-991A-4622	Sequence 4622, Ap
37	35.2	15.3	1078	2	US-08-874-186-36	Sequence 36, Appl
38	35	15.2	2082	4	US-09-818-780-67	Sequence 67, Appl
39	35	15.2	4403755	3	US-09-103-840A-2	Sequence 2, Appli
40	35	15.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
41	34.6	15.0	1308	4	US-08-937-067-18	Sequence 18, Appl
42	34.6	15.0	2078	4	US-09-087-031E-1	Sequence 1, Appli
43	34.6	15.0	4500	4	US-09-087-031E-27	Sequence 27, Appl
44	34.6	15.0	43280	2	US-08-804-227C-1	Sequence 1, Appli
45	34.4	15.0	192	4	US-09-252-991A-6732	Sequence 6732, Ap

ALIGNMENTS

RESULT 1

US-08-675-508-24

; Sequence 24, Application US/08675508

; Patent No. 5856136

; GENERAL INFORMATION:

; APPLICANT: Au-Young, Janice

; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/675,508

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0066 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 230 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

; IMMEDIATE SOURCE:

; LIBRARY: BLADTUT02

; CLONE: 13:4679

US-08-675-508-24

Query Match 100.0%; Score 230; DB 2; Length 230;

Best Local Similarity 100.0%; Pred. No. 2.6e-45;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGCTGTGACACCGACTTGTGCAACGGCAGCGGGGCCCATGCCCTGACGGCGGTGGCG 60

Db 1 GTGCTGTGACACCGACTTGTGCAACGGCAGCGGGGCCCATGCCCTGACGGCGGTGGCG 60


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; NAME/KEY: misc feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; NAME/KEY: misc feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-251-835-1

Query Match          94.5%; Score 217.4; DB 3; Length 998;
Best Local Similarity 99.1%; Pred. No. 2.5e-42;
Matches 229; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GTGCTGTGACACGACTTGTGCAAGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 60
DB 272 GTGCTGTGACACGACTTGTGCAAGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 331

QY 61 CATCTTGGCGTCTCCCTGCATCGCGCTGTCTGTGGGACCCGCCAGCTATAGGC 120
DB 332 CATCTTGGCGTCTCCCTGCATCGCGCTGTCTGTGGGACCCGCCAGCTATAGGC 391

QY 121 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTCCCGCAGGCTCTGTGCCACTCC 180
DB 392 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTCCCGCAGGCTCTGTGCCACTCC 451

QY 181 TCACAG-ACCTGGCCCGAGTGGAGCGCTGCTCTGTTCTTCTGAGGCACATCCT 230
DB 452 TCACAGAACCTGGCCCGAGTGGAGCGCTGCTCTGTTCTTCTGAGGCACATCCT 502

RESULT 7
US-09-318-503-1
; Sequence 1, Application US/09318503A
; Patent No. 6261791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318,503A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 60/074,675
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (543)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (580)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (604)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (608)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (615)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (636)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (640)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (646)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (697)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (926)
; OTHER INFORMATION: any nucleotide (i.e., a, c, g or t)
US-09-318-503-1

Query Match          94.5%; Score 217.4; DB 3; Length 998;
Best Local Similarity 99.1%; Pred. No. 2.5e-42;
Matches 229; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GTGCTGTGACACGACTTGTGCAAGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 60
DB 272 GTGCTGTGACACGACTTGTGCAAGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGC 331

QY 61 CATCTTGGCGTCTCCCTGCATCGCGCTGTCTGTGGGACCCGCCAGCTATAGGC 120
DB 332 CATCTTGGCGTCTCCCTGCATCGCGCTGTCTGTGGGACCCGCCAGCTATAGGC 391

QY 121 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTCCCGCAGGCTCTGTGCCACTCC 180
DB 392 TCTGGGGGGCCCGCTGCGAGCCACACTGGGTGTGGTCCCGCAGGCTCTGTGCCACTCC 451

QY 181 TCACAG-ACCTGGCCCGAGTGGAGCGCTGCTCTGTTCTTCTGAGGCACATCCT 230
DB 452 TCACAGAACCTGGCCCGAGTGGAGCGCTGCTCTGTTCTTCTGAGGCACATCCT 502

RESULT 8
US-09-038-261A-1
; Sequence 1, Application US/09038261A
; Patent No. 6267960
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54USU1
; CURRENT APPLICATION NUMBER: US/09/038,261A
; CURRENT FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 15
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; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,508
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT02
; CLONE: 1317088
; US-08-675-508-26

Query Match 33.5%; Score 77; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.4e-10; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 0;

QY 31 CGGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTTGGCGTGCCTCCCTGCACCTGGGCT 90
Db 1 CGGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTTGGCGTGCCTCCCTGCACCTGGGCT 60
QY 91 GCTGCTCTGGGGACCG 107
Db 61 GCTGCTCTGGGGACCG 77

RESULT 13
US-09-203-939-3
; Sequence 3, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; PRIOR FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)

US-09-203-939-3
Query Match 28.0%; Score 64.4; DB 3; Length 441;
Best Local Similarity 59.1%; Pred. No. 9.4e-07;
Matches 110; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGC 60
Db 255 GTGCTGTGACTCTGACCTGTGCAATGTCAACGGGGCCACACCTGAGGCCACCCAC 314
QY 61 CATCCTTGGCGCTGCTCCCTGCATCGCGCTGTGCTCTGGGGACCCGGCCAGTATAGGC 120
Db 315 CTTGGGGCTGCTGACCGTGTCTGTCAGCCCTGTGCTGTGGGGCTCCAGCCGCTGTGAGGC 374
QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGTGCCCGAGGCTCTGTGCCACTCC 180
Db 375 TCTGGGAGAGCCTACCATAGCCCGCATTTGTAGGGATGAGCTGCATCCACCCACCCC 434
QY 181 TCACAG 186
Db 435 ACACAG 440

RESULT 14
US-09-251-835-3
; Sequence 3, Application US/09251835A
; Patent No. 6261789
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US12
; CURRENT APPLICATION NUMBER: US/09/251,835A
; CURRENT FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)

US-09-251-835-3
Query Match 28.0%; Score 64.4; DB 3; Length 441;
Best Local Similarity 59.1%; Pred. No. 9.4e-07;
Matches 110; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGC 60
Db 255 GTGCTGTGACTCTGACCTGTGCAATGTCAACGGGGCCACACCTGAGGCCACCCAC 314
QY 61 CATCCTTGGCGCTGCTCCCTGCATCGCGCTGTGCTCTGGGGACCCGGCCAGTATAGGC 120
Db 315 CTTGGGGCTGCTGACCGTGTCTGTCAGCCCTGTGCTGTGGGGCTCCAGCCGCTGTGAGGC 374
QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGTGCCCGAGGCTCTGTGCCACTCC 180
Db 375 TCTGGGAGAGCCTACCATAGCCCGCATTTGTAGGGATGAGCTGCATCCACCCACCCC 434
QY 181 TCACAG 186
Db 435 ACACAG 440

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RESULT 15
US-09-318-503-3
; Sequence 3, Application US/09318503A
; Patent No. 6261791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318,503A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 60/074,675
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 441
; TYPE: DNA
; ORGANISM: MURINE PSCA (mpSCA)
US-09-318-503-3

Query Match      28.0%; Score 64.4; DB 3; Length 441;
Best Local Similarity 59.1%; Pred. No. 9 4e-07;
Matches 110; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY      1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGCCCCATGCCCTGCGAGCCGGCTGCCGCG 60
Db      255 GTGCTGTACTCTGACCTGTGCAATGTCAACGGGGCCCCACACCTGAAGCCACCACCAC 314
QY      61 CATCCTTGGCTGCTCCCTGCACTCGGCGCTGCTCTGGGGACCCGGCCAGCTATAGGC 120
Db      315 CTTGGGGCTGCTGACCGTCTGCACTGCTGCTGCTGCTGGGGCTCCAGCCGCTCTGTAGGC 374
QY      121 TCTGGGGGGCCCCCGCTGCGAGCCACACACTGGGTGTGTGGTGGCCCGAGGCTCTGTGCCACTCC 180
Db      375 TCTGGAGAGCCTACCATAGCCCGATTGTGAAGGGATGAGCTGCACCTCCACCCCAACCC 434
QY      181 TCACAG 186
Db      435 ACACAG 440
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Search completed: September 18, 2004, 19:23:24
Job time : 30.8687 secs

Blank Sheet


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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: BLADTUT02
CLONE: 1314679
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-934-586A-24

Query Match          100.0%; Score 230; DB 9; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-52;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCTGACAGCCGGCTGCGCGC 60
DB 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCTGACAGCCGGCTGCGCGC 60
QY 61 CATCTTGGCTGTCTCCCTGCACTCGGCTGTCTGCGGACCCCGCCAGCTATAGGC 120
DB 61 CATCTTGGCTGTCTCCCTGCACTCGGCTGTCTGCGGACCCCGCCAGCTATAGGC 120
QY 121 TCTGGGGGCCCGCTGACGCCACACTGGGTGTGTCGCCAGGCTCTGTGCCACTCC 180
DB 121 TCTGGGGGCCCGCTGACGCCACACTGGGTGTGTCGCCAGGCTCTGTGCCACTCC 180
QY 181 TCACAGACTGGCCAGTGGAGCCCTGCTCTGTTTCTCTGAGGCACATCCT 230
DB 181 TCACAGACTGGCCAGTGGAGCCCTGCTCTGTTTCTCTGAGGCACATCCT 230
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RESULT 2
US-09-080-140-6
; Sequence 6, Application US/09080140
; Publication No. US20040018553A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,140
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,653
; FILING DATE: 15-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6105.US.P1
```

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-080-140-6

Query Match          100.0%; Score 230; DB 11; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-52;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCTGACAGCCGGCTGCGCGC 60
DB 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCTGACAGCCGGCTGCGCGC 60
QY 61 CATCTTGGCTGTCTCCCTGCACTCGGCTGTCTGCGGACCCCGCCAGCTATAGGC 120
DB 61 CATCTTGGCTGTCTCCCTGCACTCGGCTGTCTGCGGACCCCGCCAGCTATAGGC 120
QY 121 TCTGGGGGCCCGCTGACGCCACACTGGGTGTGTCGCCAGGCTCTGTGCCACTCC 180
DB 121 TCTGGGGGCCCGCTGACGCCACACTGGGTGTGTCGCCAGGCTCTGTGCCACTCC 180
QY 181 TCACAGACTGGCCAGTGGAGCCCTGCTCTGTTTCTCTGAGGCACATCCT 230
DB 181 TCACAGACTGGCCAGTGGAGCCCTGCTCTGTTTCTCTGAGGCACATCCT 230
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RESULT 3
US-09-909-320-17
; Sequence 17, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-320-17

Query Match          100.0%; Score 230; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 9,1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCGGAGCGGCGCCATGCCCTGCAGCCGGCTGCCGC 60
Db 244 GTGCTGTGACACCGACTTGTGCAACGCGGAGCGGCGCCATGCCCTGCAGCCGGCTGCCGC 303
QY 61 CATCTTGGCGCTCTCCCTGCACTCGGCGCTGTCTGGGACCGCGCCAGCTATAGGC 120
Db 304 CATCTTGGCGCTCTCCCTGCACTCGGCGCTGTCTGGGACCGCGCCAGCTATAGGC 363
QY 121 TCTGGGGGGCCCCGCTGCAGCCACACTGGGTGTGGTTCCTGAGGCACATCCT 230
Db 424 TCACAGACCTGGCGCCAGTGGAGCCTGTCTCTGTTCTCTGAGGCACATCCT 473

RESULT 4
US-09-909-088B-17
; Sequence 17, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Debnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
```

```
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-088B-17

Query Match          100.0%; Score 230; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 9,1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCGGAGCGGCGCCATGCCCTGCAGCCGGCTGCCGC 60
Db 244 GTGCTGTGACACCGACTTGTGCAACGCGGAGCGGCGCCATGCCCTGCAGCCGGCTGCCGC 303
QY 61 CATCTTGGCGCTCTCCCTGCACTCGGCGCTGTCTGGGACCGCGCCAGCTATAGGC 120
Db 304 CATCTTGGCGCTCTCCCTGCACTCGGCGCTGTCTGGGACCGCGCCAGCTATAGGC 363
QY 121 TCTGGGGGGCCCCGCTGCAGCCACACTGGGTGTGGTTCCTGAGGCACATCCT 180
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Db 364 TCTGGGGGCCCCGCTGCAGCCACACTGGGTGTGTGGTCCCGCCAGGCTCTGTGCCACTCC 423
QY 181 TCACAGACTGCCCCAGTGGGAGCCTGTCTGGTTCTCTGAGGCACATCCT 230
Db 424 TCACAGACTGCCCCAGTGGGAGCCTGTCTGGTTCTCTGAGGCACATCCT 473

RESULT 5

US-09-905-291A-17
; Sequence 17, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-17

Query Match 100.0%; Score 230; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 9.1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCTCGACCGGGTGGCGC 60
Db 244 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCTCGACCGGGTGGCGC 303
QY 61 CATCTTGGCTGCTCCCTGCACTGGCCCTGCTGCTGGGACCGGCCAGCTATAGC 120
Db 304 CATCTTGGCTGCTCCCTGCACTGGCCCTGCTGCTGGGACCGGCCAGCTATAGC 363
QY 121 TCTGG 180
Db 364 TCTGG 423
QY 181 TCACAGACTGCGCCAGTGGGAGCCTGTCTGGTTCTCTGAGGCACATCCT 230
Db 424 TCACAGACTGCGCCAGTGGGAGCCTGTCTGGTTCTCTGAGGCACATCCT 473

RESULT 6

US-09-902-853-17
; Sequence 17, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26

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; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-17

Query Match      100.0%; Score 230; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 9,1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGTGCCTCC 60
Db      244  GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGTGCCTCC 303

QY      61  CATCCTTGGCGTCTCCTTGCATCTGGCGCTGTCTTCTGGGACCCGGCCAGCTATAGGC 120
Db      304  CATCCTTGGCGTCTCCTTGCATCTGGCGCTGTCTTCTGGGACCCGGCCAGCTATAGGC 363

QY      121  TCTGGGGGGCCCGCTGCAGCCACACTGGTGTGGTGGCCCGGAGGCTCTGTGCCACTCC 180
Db      364  TCTGGGGGGCCCGCTGCAGCCACACTGGTGTGGTGGCCCGGAGGCTCTGTGCCACTCC 423

QY      181  TCACAGACTGGCCCGAGTGGAGCCTGTCTGTTCTTCTGAGGCACATCCT 230
Db      424  TCACAGACTGGCCCGAGTGGAGCCTGTCTGTTCTTCTGAGGCACATCCT 473

RESULT 7
US-09-907-824-17
; Sequence 17, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-17

Query Match      100.0%; Score 230; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 9,1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGTGCCTCC 60
Db      244  GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGTGCCTCC 303

QY      61  CATCCTTGGCGTCTCCTTGCATCTGGCGCTGTCTTCTGGGACCCGGCCAGCTATAGGC 120
Db      304  CATCCTTGGCGTCTCCTTGCATCTGGCGCTGTCTTCTGGGACCCGGCCAGCTATAGGC 363

QY      121  TCTGGGGGGCCCGCTGCAGCCACACTGGTGTGGTGGCCCGGAGGCTCTGTGCCACTCC 180
Db      364  TCTGGGGGGCCCGCTGCAGCCACACTGGTGTGGTGGCCCGGAGGCTCTGTGCCACTCC 423

QY      181  TCACAGACTGGCCCGAGTGGAGCCTGTCTGTTCTTCTGAGGCACATCCT 230
Db      424  TCACAGACTGGCCCGAGTGGAGCCTGTCTGTTCTTCTGAGGCACATCCT 473
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-17

Query Match          100.0%; Score 230; DB 10; Length 960;
Best Local Similarity 100.0%; Pseq No. 9.1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1  GTGCTGTGACACCGACTTGTGTGCAACGCGCAGCGGGGGCCCATGCCCTGCGAGCCGGCTGCCGC 363
Db      244 GTGCTGTGACACCGACTTGTGTGCAACGCGCAGCGGGGGGCCCATGCCCTGCGAGCCGGCTGCCGC 363

QY      61  CATCTTGGCGTCTCCCTGCACTCGGCGCTCTCTCTCTGTGGGACCGCGCCAGCTATAGGC 120
Db      304 CATCTTGGCGTCTCCCTGCACTCGGCGCTCTCTCTCTGTGGGACCGCGCCAGCTATAGGC 363

QY      121 TCTGGGGGGCCCCGCTGCGAGCCACACTGGGTGTGGTGGCCCCCAGGCGCTCTGTGCCACTCC 230
Db      364 TCTGGGGGGCCCCGCTGCGAGCCACACTGGGTGTGGTGGCCCCCAGGCGCTCTGTGCCACTCC 473

QY      181 TCACAGACCTGGCCAGTGGGAGCGCTGTCTGGTTCCTGAGGCACATCCT 230
Db      424 TCACAGACCTGGCCAGTGGGAGCGCTGTCTGGTTCCTGAGGCACATCCT 473

RESULT 10
US-09-906-742-17
; Sequence 17, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Bctstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

```

```

; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-17

Query Match 100.0%; Score 230; DB 10; Length 960;
Best Local Similarity 100.0%; Pred.No.9.1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 GTGCTGTGACCGCACTTGTGCACGCGCAGCGGGCCCATGCCCTGCAGCGCGGTGCCGC 60
Db 244 GTGCTGTGACCGCACTTGTGCACGCGCAGCGGGCCCATGCCCTGCAGCGCGGTGCCGC 303
Qy 61 CATCCTTGCCTGTCTCCCTGCACCTCGCGCTGCTCTCTCTGGGGACCCCGCCAGCTATAGGC 120
Db 304 CATCCTTGCCTGTCTCCCTGCACCTCGCGCTGCTCTCTGGGGACCCCGCCAGCTATAGGC 363
Qy 121 TCTGGGGGGCCCGCTCGAGCCACACTGGGTGTGTTGTCGCCCGCCAGCTCTGTGCGACTCC 180
Db 364 TCTGGGGGGCCCGCTCGAGCCACACTGGGTGTGTTGTCGCCCGCCAGCTCTGTGCGACTCC 423
Qy 181 TCACAGACCTGGCCCACTGGGAGGCTGTCTCTGGTTCTCTGAGGCACATCCT 230
Db 424 TCACAGACCTGGCCCACTGGGAGGCTGTCTCTGGTTCTCTGAGGCACATCCT 473

RESULT 11

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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
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; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-613-17

Query Match 100.0%; Score 230; DB 10; Length 960;
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Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACCTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGC 60
DB 244 GTGCTGTGACACCGACCTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGC 303

QY 61 CATCCTTGGCGTGTCTCCCTGCACCTCGGCTGTGCTGTGGGACCCGCCAGCTATAGGC 120
DB 304 CATCCTTGGCGTGTCTCCCTGCACCTCGGCTGTGCTGTGGGACCCGCCAGCTATAGGC 363

QY 121 TCTGGGGGGCCCCGGCTGCAGCCACACCTGGGTGTGTCGCCCGCCAGCTCTGTGCCACTCC 180
DB 364 TCTGGGGGGCCCCGGCTGCAGCCACACCTGGGTGTGTCGCCCGCCAGCTCTGTGCCACTCC 423

QY 181 TCACAGACCTGGCCAGTGGGAGCGCTGTCTGTTCTCCTGAGGCACATCCT 230
DB 424 TCACAGACCTGGCCAGTGGGAGCGCTGTCTGTTCTCCTGAGGCACATCCT 473

RESULT 13

US-09-907-942-17
; Sequence 17, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 17
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-942-17

Query Match 100.0%; Score 230; DB 10; Length 960;
Best Local Similarity 100.0%; Pred. No. 9.1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACCTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGC 60
DB 244 GTGCTGTGACACCGACCTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCGCGCTGCCGC 303

QY 61 CATCCTTGGCGTGTCTCCCTGCACCTCGGCTGTGCTGTGGGACCCGCCAGCTATAGGC 120
DB 304 CATCCTTGGCGTGTCTCCCTGCACCTCGGCTGTGCTGTGGGACCCGCCAGCTATAGGC 363

QY 121 TCTGGGGGGCCCCGGCTGCAGCCACACCTGGGTGTGTCGCCCGCCAGCTCTGTGCCACTCC 180
DB 364 TCTGGGGGGCCCCGGCTGCAGCCACACCTGGGTGTGTCGCCCGCCAGCTCTGTGCCACTCC 423

QY 181 TCACAGACCTGGCCAGTGGGAGCGCTGTCTGTTCTCCTGAGGCACATCCT 230
DB 424 TCACAGACCTGGCCAGTGGGAGCGCTGTCTGTTCTCCTGAGGCACATCCT 473


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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR APPLICATION NUMBER: PCT/US99/30999
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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-204-17

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Best Local Similarity 100.0%; Pred. No. 9.1e-53;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTGCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCGCTGCAGCGGCTGCCGC 60
Db      244  GTGCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCGCTGCAGCGGCTGCCGC 303
QY      61  CATCCTTGCCTGTCTCCCTGCACCTCGGCTGTCTCTTGGGGACCCGGCCAGCTATAGGC 120
Db      304  CATCCTTGCCTGTCTCCCTGCACCTCGGCTGTCTCTTGGGGACCCGGCCAGCTATAGGC 363
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Db      364  TCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 423
QY      181  TCACAGACCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 230
Db      424  TCACAGACCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 473
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 05:54:35 ; Search time 1051.77 Seconds
(without alignments)
6530.246 Million cell updates/sec

Title: US-09-079-874-6

Perfect score: 230

Sequence: 1 GTCCTGTGACACGACTTCT.....TGGTTCCTGAGCACATCT 230

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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7	230	100.0	827	12	BM018750
8	230	100.0	911	13	BU194301
9	230	100.0	922	13	BU168360
10	230	100.0	924	13	BU174317
11	230	100.0	972	12	BM018834
12	230	100.0	1024	8	BCC23582
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17	223.6	97.2	901	13	BU173702
18	223.6	97.2	924	13	BQ678675
19	223.6	97.2	936	13	BU174241
20	223.6	97.2	957	13	BQ876328
21	223.6	97.2	970	13	BU179764
22	223.6	97.2	990	11	BC048808
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5', mRNA sequence.
ACCESSION
CB147558
VERSION
CB147558.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 550)
AUTHORS
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE
21C Frontier Korean EST Project 2001
JOURNAL
Unpublished (2002)
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 row: C column: 07
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CB147558 550 bp mRNA linear EST 29-JAN-2003
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VERSION
CB147558.1
KEYWORDS
EST.
SOURCE
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ORGANISM
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REFERENCE
1 (bases 1 to 550)
AUTHORS
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE
21C Frontier Korean EST Project 2001
JOURNAL
Unpublished (2002)
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
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CB147558 550 bp mRNA linear EST 29-JAN-2003
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5', mRNA sequence.
ACCESSION
CB147558
VERSION
CB147558.1
KEYWORDS
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Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 550)
AUTHORS
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE
21C Frontier Korean EST Project 2001
JOURNAL
Unpublished (2002)
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
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FEATURES
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        with tobacco acid pyrophosphatase (TAP). The decapped
        intact mRNA was ligated with DNA-RNA linker including
        EcoRI site by treatment of T4 RNA ligase and the first
        strand cDNA was synthesized from oligo dt-selected mRNA by
        priming with dt-tailed vector. The dt-tailed vector was
        adjusted to have about 60nt. The cDNA vector was
        circularized with E. coli DNA ligase after digestion of
        EcoRI which site is also included in vector. An RNA strand
        converted to a DNA strand by Okayama-Berg method. The
        obtained cDNA vectors were used for transformation of
        competent cells E. coli Top10f by electroporation method.
        The cDNA libraries constructed by this method are
        full-length enriched cDNA library. After analyzing and
        sequencing about 2,000 - 3,000 colonies in original cDNA
        library, the abundant cDNAs were selected and amplified by
        PCR reaction using vector region primer including 77
        promotor as 5' primer and Nid114 as 3' primer. The PCR
        products were used as template for synthesis of
        biotinylated single stranded RNA by in vitro transcription
        reaction. The synthesized RNA probes were hybridized with
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        library and incubated with avidin-gel. After removing
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        electroporation method."

ORIGIN
  Query Match      100.0%; Score 230; DB 14; Length 550;
  Best Local Similarity 100.0%; Pred. No. 5e-37;
  Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCGCCGCGGCTGCCGC 60
DB 272 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCGCCGCGGCTGCCGC 331
QY 61 CATCCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGCCAGCTATAGGC 120
DB 332 CATCCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGCCAGCTATAGGC 391
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DB 392 TCTGGGGGGCCCGCTGCGACCCACACTGGGTGTGGTGCCCGCCAGGCTCTGTGCCACTCC 451
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VERSION
  BI253841.1 GI:14805664
KEYWORDS
  EST.
SOURCE
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  NIH-MGC http://mgs.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  JOURNAL
  COMMENT
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-x@mail.nih.gov
    Tissue Procurement: ATCC
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
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      /clone_lib="NIH_MGC_12"
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      Technologies."

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  Query Match      100.0%; Score 230; DB 12; Length 642;
  Best Local Similarity 100.0%; Pred. No. 5.3e-37;
  Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCGCCGCGGCTGCCGC 60
DB 137 GTGCTGTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCGCCGCGGCTGCCGC 196
QY 61 CATCCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGCCAGCTATAGGC 120
DB 197 CATCCTTGGCTGCTCCCTGCACTCGGCTGTGCTGTGGGACCGCGCCAGCTATAGGC 256
QY 121 TCTGGGGGGCCCGCTGCGACCCACACTGGGTGTGGTGCCCGCCAGGCTCTGTGCCACTCC 180
DB 257 TCTGGGGGGCCCGCTGCGACCCACACTGGGTGTGGTGCCCGCCAGGCTCTGTGCCACTCC 316
QY 181 TCACAGACCTGGCCAGTGGAGCCCTGTCTGTTCTCTGAGGCACATCCT 230
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DEFINITION
  603616172F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5557096 5',
  mRNA sequence.
ACCESSION
  BM042219
VERSION
  BM042219.1 GI:16771486
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 682)
      NIH-MGC http://mgs.nci.nih.gov/
      National Institutes of Health, Mammalian Gene Collection (MGC)
      Unpublished (1999)
      JOURNAL
      COMMENT
        Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-x@mail.nih.gov
        Tissue Procurement: DCTD/Drp

Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 682)
  NIH-MGC http://mgs.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  JOURNAL
  COMMENT
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-x@mail.nih.gov
    Tissue Procurement: DCTD/Drp

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cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2021 row: o column: 17
High quality sequence stop: 678.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5557096"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life technologies). Note: this is a
NIH_MGC Library."

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source

ORIGIN
Query Match 100.0%; Score 230; DB 12; Length 682;
Best Local Similarity 100.0%; Pred. No. 5.4e-37;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGACCGCGGTGCCGC 60
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QY 61 CATCTTTGGCTGCTCCCTGCACTCGGCTGTCTCTGGGACCGCGGCACCTATAGGC 120
Db 322 CATCTTTGGCTGCTCCCTGCACTCGGCTGTCTCTGGGACCGCGGCACCTATAGGC 381
QY 121 TCTGGGGGGGGCCCGCTGACGCCACACTGGGTGTGTGTCGCCCGAGGCTCTGTGCCACTCC 180
Db 382 TCTGGGGGGGGCCCGCTGACGCCACACTGGGTGTGTGTCGCCCGAGGCTCTGTGCCACTCC 441
QY 181 TCACAGACCTGGCCAGTGGGAGCCTGTCTGTGTTCTTCTGAGGCACATCTCT 230
Db 442 TCACAGACCTGGCCAGTGGGAGCCTGTCTGTGTTCTTCTGAGGCACATCTCT 491

RESULT 4
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LOCUS 602717425F1 NIH_MGC_49 692 bp mRNA linear EST 15-MAY-2001
DEFINITION
ACCESSION BG761095
VERSION BG761095.1 GI:14071748
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: AFCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM1673 row: a column: 07
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/lab_host="DH10B (phage-resistant)"
/lab_lib="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 100.0%; Score 230; DB 12; Length 692;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 262 GTGCTGTGACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGACCGCGGTGCCGC 321
QY 61 CATCTTTGGCTGCTCCCTGCACTCGGCTGTCTCTGGGACCGCGGCACCTATAGGC 120
Db 322 CATCTTTGGCTGCTCCCTGCACTCGGCTGTCTCTGGGACCGCGGCACCTATAGGC 381
QY 121 TCTGGGGGGGGCCCGCTGACGCCACACTGGGTGTGTGTCGCCCGAGGCTCTGTGCCACTCC 180
Db 382 TCTGGGGGGGGCCCGCTGACGCCACACTGGGTGTGTGTCGCCCGAGGCTCTGTGCCACTCC 441
QY 181 TCACAGACCTGGCCAGTGGGAGCCTGTCTGTGTTCTTCTGAGGCACATCTCT 230
Db 442 TCACAGACCTGGCCAGTGGGAGCCTGTCTGTGTTCTTCTGAGGCACATCTCT 491

RESULT 5

BG041997
LOCUS 60361580F1 NIH_MGC_112 735 bp mRNA linear EST 07-NOV-2001
DEFINITION
ACCESSION BG041997
VERSION BG041997.1 GI:16771264
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 735)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 733.
Location/Qualifiers
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/organism="Homo sapiens"

FEATURES
source

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/mol_type="mrna"
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/clone="IMAGE:5420779"
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/lab_host="PH103 (phage-resistant)"
/clone_lib="NIH_MGC_112"
/notes="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match 100.0%; Score 230; DB 12; Length 735;
Best Local Similarity 100.0%; Pred. No. 5.6e-37;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCGCTGCAGCGGCTGCCGC 60
Db 174 GTGCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCGCTGCAGCGGCTGCCGC 233
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Db 234 CATCTTGGCGTGTCTCCCTGCACTGGCGCTGTCTGGGACCGCGGCAGCTATAGGC 293
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Db 294 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGTGCCCGCCAGCCTCTGCGCACTCC 353
QY 181 TCACAGACTGGCCAGTGGGAGCGCTGCTGTTCTCTGAGGCACATCCT 230
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RESULT 6
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LOCUS 602738887F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4868924 5',
DEFINITION mrna sequence.
ACCESSION BG765417
VERSION BG765417.1 GI:14076070
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ARCC/DCRP/BTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1739 row: m column: 21
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FEATURES
source

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/notes="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.6e-37;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCGCTGCAGCGGCTGCCGC 60
Db 256 GTGCTGTGACACGACTTGTGCAACGCCAGCGGGGCCCATGCGCTGCAGCGGCTGCCGC 315
QY 61 CATCTTGGCGTGTCTCCCTGCACTGGCGCTGTCTGGGACCGCGGCAGCTATAGGC 120
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QY 121 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGTGCCCGCCAGCCTCTGTGCCACTCC 180
Db 376 TCTGGGGGGCCCGCTGCAGCCACACTGGGTGTGGTGTGCCCGCCAGCCTCTGTGCCACTCC 435
QY 181 TCACAGACTGGCCAGTGGGAGCGCTGCTGTTCTCTGAGGCACATCCT 230
Db 436 TCACAGACTGGCCAGTGGGAGCGCTGCTGTTCTCTGAGGCACATCCT 485
RESULT 7
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LOCUS 603646552F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5428261 5',
DEFINITION mrna sequence.
ACCESSION BG018750
VERSION BG018750.1 GI:165333104
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1895 row: g column: 14
High quality sequence stop: 810.
Location/Qualifiers
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/notes="Organ: brain; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of

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